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UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 C.F.R. § 1.53(b))

Attorney Docket No.	HB1-0003
First Inventor or Application Identifier	Heard
Title	Plant Gene Sequence I
Express Mail Label No.	EJ498962678 US

APPLICATION ELEMENTS See MPEP chapter 600 concerning utility patent application contents.

ADDRESS TO: Assistant Commissioner for Patents
Box Patent Application
Washington, DC 20231

- ☒ Fee Transmittal Form (e.g., PTO/SB/17)
(Submit an original and a duplicate for fee processing)
- ☒ Specification [Total Pages 43]
(preferred arrangement set forth below)
 - Descriptive title of the Invention
 - Cross References to Related Applications
 - Statement Regarding Fed sponsored R & D
 - Reference to Microfiche Appendix
 - Background of the Invention
 - Brief Summary of the Invention
 - Brief Description of the Drawings (if filed)
 - Detailed Description
 - Claim(s)
 - Abstract of the Disclosure
- ☐ Drawing(s) (35 U.S.C. 113) [Total Sheets ☐
- Oath or Declaration [Total Pages ☐]
 - ☒ Newly executed (original or copy)
 - ☐ Copy from a prior application (37 C.F.R. § 1.63(d))
(for continuation/divisional with Box 16 completed)
 - ☐ DELETION OF INVENTOR(S)
Signed statement attached deleting inventor(s) named in the prior application, see 37 C.F.R. §§ 1.63(d)(2) and 1.33(b).

- ☐ Microfiche Computer Program (Appendix)
- Nucleotide and/or Amino Acid Sequence Submission (if applicable, all necessary)
 - ☒ Computer Readable Copy
 - ☒ Paper Copy (identical to computer copy)
 - ☒ Statement verifying identity of above copies

* NOTE FOR ITEMS 1 & 13: IN ORDER TO BE ENTITLED TO PAY SMALL ENTITY FEES, A SMALL ENTITY STATEMENT IS REQUIRED (37 C.F.R. § 1.27), EXCEPT IF ONE FILED IN A PRIOR APPLICATION IS RELIED UPON (37 C.F.R. § 1.28).

ACCOMPANYING APPLICATION PARTS

- ☒ Assignment Papers (cover sheet & document(s))
- ☒ 37 C.F.R. §3.73(b) Statement (when there is an assignee) ☒ Power of Attorney
- ☐ English Translation Document (if applicable)
- ☐ Information Disclosure Statement (IDS)/PTO-1449 ☐ Copies of IDS Citations
- ☐ Preliminary Amendment
- ☐ Return Receipt Postcard (MPEP 503)
(Should be specifically itemized)
- ☒ Small Entity Statement(s) ☐ Statement filed in prior application, Status still proper and desired (PTO/SB/09-12)
- ☐ Certified Copy of Priority Document(s) (if foreign priority is claimed)
- Other: _____

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17. CORRESPONDENCE ADDRESS

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application

Inventor(s): Jacqueline Heard et al.

Application No.: Unassigned

Filed: Herewith

Title: Plant Gene Sequences I

VERIFIED STATEMENT CLAIMING SMALL ENTITY STATUS
37 C.F.R. § 1.9(i) AND 1.27(c) - SMALL BUSINESS CONCERN

I hereby declare that I am an official of the small business concern empowered to act on behalf of the concern identified below.

Name: Mendel Biotechnology, Inc.

Address: 21375 Cabot Boulevard, Hayward, California 94545

I hereby declare that the above identified small business concern qualifies as a small business concern as defined in 13 C.F.R. § 121.12, and reproduced in 37 C.F.R. § 1.9(d), for purposes of paying reduced fees under Section 41(a) and (b) of Title 35 U.S.C. in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third-party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention.

entitled: Plant Gene Sequences I

described in the Specification filed herewith

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If the rights held by the above-identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below and no rights to the invention are held by any person, other than the inventor, who could not qualify as a small business concern under 37 C.F.R. § 1.9(d) or by any concern which would not qualify as a small business concern under 37 C.F.R. § 1.9(d) or a nonprofit organization under 37 C.F.R. § 1.9(e).

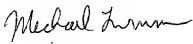
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☐ Individual ☐ SmallBusinessConcern ☐ Nonprofit Organization

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small business entity is no longer appropriate. (37 C.F.R. § 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

Name of Person Signing: Michael Fromm
 Title of Person Signing: President and CEO
 Address of Person Signing: 21375 Cabot Boulevard, Hayward, California 94545
 Signature: 
 Date: 9/8/99

00354519.001369

PLANT GENE SEQUENCES I

The present invention claims priority in part from Provisional Application
Serial Nos. 60/101,349, filed September 22, 1998; 60/103,312, filed October 6,
5 1998; 60/108,734, filed November 17, 1998; and 60/113,409, filed December 22,
1998.

FIELD OF THE INVENTION

This invention is in the field of plant molecular biology and relates to
10 compositions and methods for modifying a plant's traits.

BACKGROUND OF THE INVENTION

Gene expression levels are controlled in part at the level of transcription,
and transcription is affected by transcription factors. Transcription factors regulate
15 gene expression throughout the life cycle of an organism and so are responsible for
differential levels of gene expression at various developmental stages, in different
tissue and cell types, and in response to different stimuli. Transcription factors
may interact with other proteins or with specific sites on a target gene sequence to
activate, suppress or otherwise regulate transcription. In addition, the transcription
20 of the transcription factors themselves may be regulated.

Because transcription factors are key controlling elements for biological
pathways, altering the expression levels of one or more transcription factors may
change entire biological pathways in an organism. For example, manipulation of
the levels of selected transcription factors may result in increased expression of
25 economically useful proteins or metabolic chemicals in plants or to improve other
agriculturally relevant characteristics. Conversely, blocked or reduced expression
of a transcription factor may reduce biosynthesis of unwanted compounds or
remove an undesirable trait. Therefore, manipulating transcription factor levels in
a plant offers tremendous potential in agricultural biotechnology for modifying a
30 plant's traits.

The present invention provides novel transcription factors for use in
modifying a plant's traits

SUMMARY OF THE INVENTION

In one aspect, the present invention relates to an isolated polynucleotide comprising a nucleotide sequence encoding a transcription factor. In one embodiment, the polynucleotide is a sequence provided in the Sequence Listing as

5 SEQ ID No. 1 (G4), SEQ ID No. 3 (G5), SEQ ID No. 5 (G8), SEQ ID No. 7 (G9), SEQ ID No. 9 (G10), SEQ ID No. 11 (G14), SEQ ID No. 13 (G864), SEQ ID No. 15 (G865), SEQ ID No. 17 (G867), SEQ ID No. 19 (G869), SEQ ID No. 21 (G872), SEQ ID No. 23 (G971), SEQ ID No. 25 (G974), SEQ ID No. 27 (G975), SEQ ID No. 29 (G976), SEQ ID No. 31 (G977), SEQ ID No. 33 (G979), SEQ ID

10 No. 35 (G993), SEQ ID No. 37 (G1020), SEQ ID No. 39 (G1023), SEQ ID No. 41 (G661), SEQ ID No. 43 (G663), SEQ ID No. 45 (G664), SEQ ID No. 47 (G672), SEQ ID No. 49 (G673), SEQ ID No. 51 (G675), SEQ ID No. 53 (G677), SEQ ID No. 55 (G679), SEQ ID No. 57 (G932), SEQ ID No. 59 (G994), SEQ ID No. 61 (G996), SEQ ID No. 63 (G997), SEQ ID No. 65 (G1328), SEQ ID No. 67 (G858),

15 SEQ ID No. 69 (G860), SEQ ID No. 71 (G861), SEQ ID No. 73 (G866), SEQ ID No. 75 (G877), SEQ ID No. 77 (G878), SEQ ID No. 79 (G883), SEQ ID No. 81 (G884), SEQ ID No. 83 (G920), SEQ ID No. 85 (G921), SEQ ID No. 87 (G986), SEQ ID No. 89 (G1022), SEQ ID No. 91 (G1043), SEQ ID No. 93 (G1091), SEQ ID No. 95 (G837), SEQ ID No. 97 (G838), SEQ ID No. 99 (G850), SEQ ID No.

20 101 (G1241), SEQ ID No. 103 (G749), SEQ ID No. 105 (G751), SEQ ID No. 107 (G897), SEQ ID No. 109 (G902), SEQ ID No. 111 (G905), SEQ ID No. 113 (G908), SEQ ID No. 115 (G909), SEQ ID No. 117 (G911), SEQ ID No. 119 (G1255), SEQ ID No. 121 (G1258), SEQ ID No. 123 (G399), SEQ ID No. 125 (G699), SEQ ID No. 127 (G964), SEQ ID No. 129 (G1334), SEQ ID No. 131 (G718), SEQ ID No. 133 (G763), SEQ ID No. 135 (G462), SEQ ID No. 137 (G782), SEQ ID No. 139 (G783), SEQ ID No. 141 (G786), SEQ ID No. 143 (G793), SEQ ID No. 145 (G801), SEQ ID No. 147 (G802), SEQ ID No. 149 (G1065), SEQ ID No. 151 (G629), SEQ ID No. 153 (G630), SEQ ID No. 155 (G735), SEQ ID No. 157 (G1034), SEQ ID No. 159 (G1035), SEQ ID No. 161 (G1048), SEQ ID No. 163 (G1058), SEQ ID No. 165 (G849), SEQ ID No. 167 (G726), or SEQ ID No. 169 (G1197).

In another embodiment, the polynucleotide of the invention is one that is homologous to a polynucleotide provided in the Sequence Listing as determined under stringent hybridization conditions or by the analysis of sequence identity

criteria. In yet another embodiment, the polynucleotide may comprise a sequence comprising a fragment of at least 15 consecutive nucleotides of a polynucleotide sequence of the invention. The polynucleotide may further comprise a promoter operably linked to the sequence. The promoter may be a constitutive, an inducible or a tissue-active promoter.

In a second aspect, the present invention relates to an isolated polypeptide that is a transcription factor. In one embodiment, the polypeptide comprises a sequence provided in the Sequence Listing as SEQ ID No. 2 (G4 prot), SEQ ID No. 4 (G5 prot), SEQ ID No. 6 (G8 prot), SEQ ID No. 8 (G9 prot), SEQ ID No. 10 (G10 prot), SEQ ID No. 12 (G14 prot), SEQ ID No. 14 (G864 prot), SEQ ID No. 16 (G865 prot), SEQ ID No. 18 (G867 prot), SEQ ID No. 20 (G869 prot), SEQ ID No. 22 (G872 prot), SEQ ID No. 24 (G971 prot), SEQ ID No. 26 (G974 prot), SEQ ID No. 28 (G975 prot), SEQ ID No. 30 (G976 prot), SEQ ID No. 32 (G977 prot), SEQ ID No. 34 (G979 prot), SEQ ID No. 36 (G993 prot), SEQ ID No. 38 (G1020 prot), SEQ ID No. 40 (G1023 prot), SEQ ID No. 42 (G661 prot), SEQ ID No. 44 (G663 prot), SEQ ID No. 46 (G664 prot), SEQ ID No. 48 (G672 prot), SEQ ID No. 50 (G673 prot), SEQ ID No. 52 (G675 prot), SEQ ID No. 54 (G677 prot), SEQ ID No. 56 (G679 prot), SEQ ID No. 58 (G932 prot), SEQ ID No. 60 (G994 prot), SEQ ID No. 62 (G996 prot), SEQ ID No. 64 (G997 prot), SEQ ID No. 66 (G1328 prot), SEQ ID No. 68 (G858 prot), SEQ ID No. 70 (G860 prot), SEQ ID No. 72 (G861 prot), SEQ ID No. 74 (G866 prot), SEQ ID No. 76 (G877 prot), SEQ ID No. 78 (G878 prot), SEQ ID No. 80 (G883 prot), SEQ ID No. 82 (G884 prot), SEQ ID No. 84 (G920 prot), SEQ ID No. 86 (G921 prot), SEQ ID No. 88 (G986 prot), SEQ ID No. 90 (G1022 prot), SEQ ID No. 92 (G1043 prot), SEQ ID No. 94 (G1091 prot), SEQ ID No. 96 (G837 prot), SEQ ID No. 98 (G838 prot), SEQ ID No. 100 (G850 prot), SEQ ID No. 102 (G1241), SEQ ID No. 104 (G749 prot), SEQ ID No. 106 (G751 prot), SEQ ID No. 108 (G897 prot), SEQ ID No. 110 (G902 prot), SEQ ID No. 112 (G905 prot), SEQ ID No. 114 (G908 prot), SEQ ID No. 116 (G909 prot), SEQ ID No. 118 (G911 prot), SEQ ID No. 120 (G1255 prot), SEQ ID No. 122 (G1258 prot), SEQ ID No. 124 (G399 prot), SEQ ID No. 126 (G699 prot), SEQ ID No. 128 (G964 prot), SEQ ID No. 130 (G1334 prot), SEQ ID No. 132 (G718 prot), SEQ ID No. 134 (G763 prot), SEQ ID No. 136 (G462 prot), SEQ ID No. 138 (G782 prot), SEQ ID No. 140 (G783 prot), SEQ ID No. 142 (G786 prot), SEQ ID No. 144 (G793 prot), SEQ ID No. 146 (G801

prot), SEQ ID No. 148 (G802 prot), SEQ ID No. 150 (G1065 prot), SEQ ID No. 152 (G629 prot), SEQ ID No. 154 (G630 prot), SEQ ID No. 156 (G735 prot), SEQ ID No. 158 (G1034 prot), SEQ ID No. 160 (G1035 prot), SEQ ID No. 162 (G1048 prot), SEQ ID No. 164 (G1058 prot), SEQ ID No. 166 (G849 prot), SEQ ID No. 168 (G726 prot), or SEQ ID No. 170 (G1197 prot).

In another embodiment, the polypeptide comprises a sequence with one or more substitutions, deletions or insertions to a sequence provided in the Sequence Listing or a sequence which when ectopically expressed in a plant modifies a plant trait in a similar manner as a sequence provided in the Sequence Listing. The polypeptide may also comprise a fragment of at least 6 consecutive amino acids of a sequence provided in the Sequence Listing.

The invention also comprises an expression vector comprising a polynucleotide described above, a host cell comprising the expression vector or a transgenic plant comprising an isolated polynucleotide or polypeptide described above.

The invention also provides a method for producing a transgenic plant comprising an isolated polynucleotide or polypeptide described above. The method comprises (a) ectopically expressing an isolated polynucleotide encoding a polypeptide of the invention in a plant; and (b) selecting a plant expressing the polynucleotide.

In another aspect the invention provides a method for screening for one or more molecules to identify a molecule that modifies the expression of a polynucleotide or polypeptide of the invention in a plant. The method entails (a) placing the molecule in contact with the plant; and (b) monitoring the effect of the molecule on the expression of the polynucleotide or polypeptide in the plant.

In yet another aspect, the invention provides a method for identifying a sequence homologous to a polynucleotide or polypeptide sequence provided in the Sequence Listing. The method comprises (a) providing a database sequence; (b) aligning and comparing the sequence provided with the database sequence to determine whether the database sequence meets sequence identity criteria relative to the sequence provided herein; and (c) selecting any database sequence that meets the sequence identity criteria. The present invention also encompasses a homologous polypeptide or polynucleotide identified by the method and a transgenic plant comprising the homologous sequence.

The invention further provides a method for screening for a transcription factor that modifies a plant trait, said method comprising (a) generating one or more transgenic plants ectopically expressing an isolated polynucleotide of claim 1 and (b) identifying from said generated transgenic plants a plant with a modified plant trait.

DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

A “polynucleotide” is a nucleotide sequence comprising a gene coding sequence or a fragment thereof (comprising at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides, and more preferably at least 50 consecutive nucleotides), a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation site, 5’ or 3’ untranslated regions, a reporter gene, a selectable marker or the like. The polynucleotide may comprise single stranded or double stranded DNA or RNA. The polynucleotide may comprise modified bases or a modified backbone. The polynucleotide may be genomic, a transcript (such as an mRNA) or a processed nucleotide sequence (such as a cDNA). The polynucleotide may comprise a sequence in either sense or antisense orientations.

An “isolated polynucleotide” is a polynucleotide that is not in its native state, e.g., the polynucleotide is comprised of a nucleotide sequence not found in nature or the polynucleotide is separated from nucleotide sequences with which it typically is in proximity or is next to nucleotide sequences with which it typically is not in proximity.

An “isolated polypeptide” is a polypeptide derived from the translation of an isolated polynucleotide or is more enriched in a cell than the polypeptide in its natural state in a wild type cell, e.g. more than 5% enriched, more than 10% enriched or more than 20% enriched and is not the result of a natural response of a wild type plant or is separated from other components with which it is typically associated with in a cell.

A “transgenic plant” refers to a plant that contains genetic material not normally found in a wild type plant of the same species, or in a naturally occurring variety or in a cultivar, and which has been introduced into the plant by human

manipulation. A transgenic plant is a plant that may contain an expression vector or cassette. The expression cassette comprises a gene coding sequence and allows for the expression of the gene coding sequence. The expression cassette may be introduced into a plant by transformation or by breeding after transformation of a parent plant.

The transgenic plant may comprise machinery, such as the T-DNA activation tagging machinery, necessary for ectopically expressing an endogenous gene coding sequence. T-DNA activation tagging entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has been inserted in the genome, expression of a flanking gene coding sequence becomes deregulated (Ichikawa et al., (1997) *Nature* 390: 698-701; Kakimoto et al., *Science* 274: 982-985 (1996)). The transgenic plant may also comprise the machinery necessary for expressing or altering the activity of a polypeptide encoded by an endogenous gene, for example by altering the phosphorylation state of the polypeptide to maintain it in an activated state. A transgenic plant refers to a whole plant as well as to a plant part, such as seed, fruit, leaf, or root, plant tissue, plant cells or any other plant material, and progeny thereof.

The phrase “ectopically expressed” in reference to polynucleotide or polypeptide expression refers to an expression pattern in the transgenic plant that is different from the expression pattern in the wild type plant or a reference; for example, by expression in a cell type other than a cell type in which the sequence is expressed in the wild type plant, or by expression at a time other than at the time the sequence is expressed in the wild type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at different expression levels (either higher or lower) compared with those found in a wild type plant. The term also refers to lowering the levels of expression to below the detection level or completely abolishing expression. The resulting expression pattern may be transient or stable.

A “transcription factor” (TF) refers to a polypeptide that controls the expression of a gene or genes either directly by binding to one or more nucleotide sequences associated with a gene coding sequence or indirectly by affecting the level or activity of other polypeptides that do bind directly to one or more nucleotide sequences associated with a gene coding sequence. A transcription factor may activate or repress expression of a gene or genes.

The transcription factor sequence may comprise a whole coding sequence or a fragment or domain of a coding sequence. A "fragment or domain", as referred to polypeptides, may be a portion of a polypeptide which performs at least one biological function of the intact polypeptide in substantially the same manner or to a similar extent as does the intact polypeptide, e.g. those fragments provided in Table 1. A fragment may comprise, for example, a DNA binding domain that binds to a specific DNA binding region, an activation domain or a domain for protein-protein interactions. Fragments may vary in size from as few as 6 amino acids to the length of the intact polypeptide, but are preferably at least 30 amino acids in length and more preferably 60 amino acids in length. In reference to a nucleotide sequence "a fragment" refers to any sequence of at least consecutive 15 nucleotides, preferably at least 30 nucleotides, more preferably at least 50, of any of the sequences provided herein and as an example include nucleotides 1-100, 101-200, 201-300, 501-600, 801-900, 1000-1015, or 1101-1300 of SEQ ID No. 1.

"Trait" refers to a physiological, morphological, biochemical or physical characteristic of a plant or particular plant material or cell. This characteristic may be visible to the human eye, such as seed or plant size, or be measured by biochemical techniques, such as the protein, starch or oil content of seed or leaves or by the observation of the expression level of genes by employing Northern, RT PCR, microarray gene expression assays or reporter gene expression systems or be measured by agricultural observations such as stress tolerance, yield or disease resistance.

"Trait modification" refers to a detectable difference in a characteristic in a transgenic plant ectopically expressing a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild type plant. The trait modification may entail at least a 5% increase or decrease in an observed trait (difference), at least a 10% difference, at least a 20% difference, at least a 30%, at least a 50%, at least a 70%, at least a 100% or a greater difference. It is known that there may be a natural variation in the modified trait. Therefore, the trait modification observed entails a change of the normal distribution of the trait in transgenic plants compared with the distribution observed in wild type plant.

Trait modifications of particular interest include those to seed (embryo), fruit, root, flower, leaf, stem, shoot, seedling or the like, including: enhanced tolerance to environmental conditions including freezing, chilling, heat, drought,

water saturation, radiation and ozone; enhanced resistance to microbial, fungal or viral diseases; decreased herbicide sensitivity, enhanced tolerance of heavy metals (or enhanced ability to take up heavy metals), enhanced growth under poor photoconditions (e.g., low light and/or short day length), or changes in expression levels of genes of interest. Other phenotype that may be modified relate to the production of plant metabolites, such as variations in the production of taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, antioxidants, amino acids, lignins, cellulose, tannins, prennylipids (such as chlorophylls and carotenoids), glucosinolates, and terpenoids, enhanced or compositionally altered protein or oil production (especially in seeds), or modified sugar (insoluble or soluble) and/or starch composition. Physical plant characteristics that may be modified include cell development (such as the number of trichomes), fruit and seed size and number, yields of plant parts such as stems, leaves and roots, the stability of the seeds during storage, characteristics of the seed pod (e.g., susceptibility to shattering), root hair length and quantity, internode distances, or the quality of seed coat. Plant growth characteristics that may be modified include growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, biomass or transpiration characteristics, as well as plant architecture characteristics such as apical dominance, branching patterns, number of organs, organ identity, organ shape or size.

1. The Sequences

We have discovered novel polynucleotides and polypeptides that are plant transcription factors. The plant transcription factors are derived from *Arabidopsis thaliana* and belong to one of the following transcription factor families: the AP2 (APETALA2) domain transcription factor family (Riechmann and Meyerowitz (1998) *J. Biol. Chem.* 379:633-646); the MYB transcription factor family (Martin and Paz-Ares, (1997) *Trends Genet.* 13:67-73); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) *J. Biol. Chem.* 378:1079-1101); the WRKY protein family (Ishiguro and Nakamura (1994) *Mol. Gen. Genet.* 244:563-571); the ankyrin-repeat protein family (Zhang et al. (1992) *Plant Cell* 4:1575-1588); the miscellaneous protein (MISC) family (Kim et al. (1997) *Plant J.* 11:1237-1251); the zinc finger protein (Z) family (Klug and Schwabe (1995)

FASEB J. 9: 597-604); the homeobox (HB) protein family (Duboule (1994) *Guidebook to the Homeobox Genes*, Oxford University Press); the CAAT-element binding proteins (Forsburg and Guarente (1989) *Genes Dev.* 3:1166-1178); the squamosa promoter binding proteins (SPB) (Klein et al. (1996) *Mol. Gen. Genet.* 1996 250:7-16); the NAM protein family; the IAA/AUX proteins (Rouse et al. (1998) *Science* 279:1371-1373); the HLH/MYC protein family (Littlewood et al. (1994) *Prot. Profile* 1:639-709); the DNA-binding protein (DBP) family (Tucker et al. (1994) *EMBO J.* 13:2994-3002); the bZIP family of transcription factors (Foster et al. (1994) *FASEB J.* 8:192-200); the BPF-1 protein (Box P-binding factor) family (da Costa e Silva et al. (1993) *Plant J.* 4:125-135); and the golden protein (GLD) family (Hall et al. (1998) *Plant Cell* 10:925-936

The novel polynucleotides and polypeptides are provided in the Sequence Listing and are tabulated in Table 1. Table 1 identifies a SEQ ID No., its corresponding GID number, the transcription factor family to which the sequence belongs, fragments derived from the sequences and whether the sequence is a polynucleotide or a polypeptide sequence. Producing transgenic plants with modified expression levels of one or more of these transcription factors compared with those levels found in a wild type plant may be used to modify a plant's traits. The effect of modifying the expression levels of a particular transcription factor on the traits of a transgenic plant is described further in the Examples.

We have also identified domains or fragments derived from the sequences. The numbers indicating the fragment location for the cDNA sequences may be from either 5' or 3' end of the cDNA. For the protein sequences the fragment location is determined from the N-terminus of the protein and may include adjacent amino acid sequences, such as for example for SEQ ID No. 2 an additional 10, 20, 40, 60 or 100 amino acids in either N-terminal or C-terminal direction of the polypeptide.

10

SEQ ID No.	GID No. (Family)	Fragments	CDNA or protein
1	G4 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	CDNA
2	G4 (AP2)	121-188	Protein
3	G5 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	CDNA
4	G5 (AP2)	149-216	Protein
5	G8 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	CDNA
6	G8 (AP2)	151-0217 and 243-295	Protein
7	G9 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	CDNA
8	G9 (AP2)	62-127	protein
9	G10 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
10	G10 (AP2)	21-88	protein
11	G14 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
12	G14 (AP2)	122-189	protein
13	G864 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
14	G864 (AP2)	119-186	protein
15	G865 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
16	G865 (AP2)	36-103	protein
17	G867 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
18	G867 (AP2)	59-124	protein
19	G869 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
20	G869 (AP2)	110-177	protein
21	G872 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
22	G872 (AP2)	18-85	protein
23	G971 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
24	G971 (AP2)	120-186	protein
25	G974 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
26	G974 (AP2)	80-147	protein
27	G975 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
28	G975 (AP2)	4-71	protein
29	G976 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
30	G976 (AP2)	86-153	protein
31	G977 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
32	G977 (AP2)	5-72	protein
33	G979 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
34	G979 (AP2)	63-139 and 165-233	protein
35	G993 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
36	G993 (AP2)	69-134	protein
37	G1020 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
38	G1020 (AP2)	28-95	protein
39	G1023 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
40	G1023 (AP2)	128-195	protein
41	G661 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
42	G661 (MYB)	12-117	protein
43	G663 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
44	G663 (MYB)	8-112	protein
45	G664 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
46	G664 (MYB)	12-116	protein
47	G672 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
48	G672 (MYB)	90-160	protein
49	G673 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
50	G673 (MYB)	36-123	protein
51	G675 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
52	G675 (MYB)	12-126	protein

53	G677 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
54	G677 (MYB)	12-116	protein
55	G679 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
56	G679 (MYB)	98-166	protein
57	G932 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
58	G932 (MYB)	12-112	protein
59	G994 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
60	G994 (MYB)	13-111	protein
61	G996 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
62	G996 (MYB)	12-104	protein
63	G997 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
64	G997 (MYB)	11-36	protein
65	G1328 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
66	G1328 (MYB)	13-114	protein
67	G858 (MADS)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
68	G858 (MADS)	2-57	protein
69	G860 (MADS)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
70	G860 (MADS)	2-57	protein
71	G861 (MADS)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
72	G861 (MADS)	2-57	protein
73	G866 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
74	G866 (WRKY)	243-300	protein
75	G877 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
76	G877 (WRKY)	273-328 and 487-543	protein
77	G878 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
78	G878 (WRKY)	250-305 and 415-471	protein
79	G883 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
80	G883 (WRKY)	249-306	protein
81	G884 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
82	G884 (WRKY)	229-284 and 409-465	protein
83	G920 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
84	G920 (WRKY)	152-211	protein
85	G921 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
86	G921 (WRKY)	146-203	protein
87	G986 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
88	G986 (WRKY)	146-203	protein
89	G1022 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
90	G1022 (WRKY)	281-338	protein
91	G1043 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
92	G1043 (WRKY)	119-179	protein
93	G1091 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
94	G1091 (WRKY)	262-319	protein
95	G837 (AKR)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
96	G837 (AKR)	362-412	protein
97	G838 (AKR)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
98	G838 (AKR)	279-321	protein
99	G850 (MISC)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
100	G850 (MISC)	491-517	protein
101	G1241 (MISC)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
102	G1241 (MISC)	-----	protein
103	G749 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
104	G749 (Z)	125-143	protein
105	G751 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
106	G751 (Z)	37-82	protein
107	G897 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
108	G897 (Z)	8-90	protein
109	G902 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
110	G902 (Z)	56-91	protein

111	G905 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
112	G905 (Z)	118-160	protein
113	G908 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
114	G908 (Z)	8-29 and 72-88	protein
115	G909 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
116	G909 (Z)	17-68	protein
117	G911 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
118	G911 (Z)	86-129	protein
119	G1255 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
120	G1255 (Z)	17-54	protein
121	G1258 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
122	G1258 (Z)	57-108	protein
123	G399 (HB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
124	G399 (HB)	160-181	protein
125	G699 (HB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
126	G699 (HB)	89-108	protein
127	G964 (HB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
128	G964 (HB)	160-179	protein
129	G1334 (CAAT)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
130	G1334 (CAAT)	137-188	protein
131	G718 (SPBP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
132	G718 (SPBP)	176-244	protein
133	G763 (NAM)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
134	G763 (NAM)	14-160	protein
135	G462 (IAA/AUX)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
136	G462 (IAA/AUX)	11-20, 67-82, 98-131, 152-181	protein
137	G782 (HLH/MYC)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
138	G782 (HLH/MYC)	9-28	protein
139	G783 (HLH/MYC)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
140	G783 (HLH/MYC)	31-46	protein
141	G786 (HLH/MYC)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
142	G786 (HLH/MYC)	220-242	protein
143	G793 (HLH/MYC)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
144	G793 (HLH/MYC)	182-206	protein
145	G801 (DBP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
146	G801 (DBP)	51-68	protein
147	G802 (DBP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
148	G802 (DBP)	80-97	protein
149	G1065 (DBP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
150	G1065 (DBP)	146-167	protein
151	G629 (bZIP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
152	G629 (bZIP)	100-125	protein
153	G630 (bZIP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
154	G630 (bZIP)	80-105	protein
155	G735 (bZIP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
156	G735 (bZIP)	160-185	protein
157	G1034 (bZIP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
158	G1034 (bZIP)	109-134	protein
159	G1035 (bZIP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
160	G1035 (bZIP)	47-72	protein
161	G1048 (bZIP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
162	G1048 (bZIP)	150-175	protein
163	G1058 (bZIP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
164	G1058 (bZIP)	299-324	protein
165	G849 (BPF)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
166	G849 (BPF)	509-583	protein
167	G726 (GLD)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
168	G726 (GLD)	20-69	protein

169	G1197 (GLD)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
170	G1197 (GLD)	42-90	protein

The identified polypeptide fragments may be combined with fragments or sequences derived from other transcription factors so as to generate additional novel sequences, such as by employing the methods described in Short, PCT publication WO9827230, entitled "Methods and Compositions for Polypeptide Engineering" or in Patten et al., PCT publication WO9923236, entitled "Method of DNA Shuffling".

The identified polynucleotide fragments are useful as nucleic acid probes and primers. A nucleic acid probe is useful in hybridization protocols, including protocols for microarray experiments. Primers may be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods. See Sambrook et al., *Molecular Cloning. A Laboratory Manual*, Ed. 2, Cold Spring Harbor Laboratory Press, New York (1989) and Ausubel et al. (eds) *Current Protocols in Molecular Biology*, John Wiley & Sons (1998).

2. Identification of Homologous Sequences (Homologs)

Homologous sequences to those provided in the Sequence Listing derived from *Arabidopsis thaliana* or from other plants may be used to modify a plant trait. Homologous sequences may be derived from any plant including monocots and dicots and in particular agriculturally important plant species, including but not limited to, crops such as soybean, wheat, corn, potato, cotton, rice, oilseed rape (including canola), sunflower, alfalfa, sugarcane and turf; or fruits and vegetables, such as banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, brussel sprouts and kohlrabi). Other crops, fruits and vegetables whose phenotype may be changed include barley, currant, avocado, citrus fruits such as oranges, lemons,

grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, sweet potato and beans. The homologs may also be derived from woody species, such as pine, poplar and eucalyptus.

5 Substitutions, deletions and insertions introduced into the sequences provided in the Sequence Listing are also envisioned by the invention. Such sequence modifications can be engineered into a sequence by site-directed mutagenesis (Wu (ed.) *Meth. Enzymol.* (1993) vol. 217, Academic Press). Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about
10 from 1 to 30 residues. In preferred embodiments, deletions or insertions are made in adjacent pairs, e.g., a deletion of two residues or insertion of two residues. Substitutions, deletions, insertions or any combination thereof may be combined to arrive at a sequence. The mutations that are made in the polynucleotide encoding
15 the transcription factor should not place the sequence out of reading frame and should not create complementary regions that could produce secondary mRNA structure. Preferably, the polypeptide encoded by the DNA should perform the desired function.

20 Substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the following Table 2 when it is desired to maintain the activity of the protein. Table 2 shows amino acids which may be substituted for an amino acid in a protein and which are typically regarded as conservative substitutions.

Table 2

Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln; His
Asp	Glu
Gln	Asn
Cys	Ser
Glu	Asp
Gly	Pro
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr; Gly
Thr	Ser; Val
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

Substitutions that are less conservative than those in Table 2 may be selected by picking residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl,

or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

Additionally, the term “homologous sequence” encompasses a polypeptide sequence that is modified by chemical or enzymatic means. The homologous sequence may be a sequence modified by lipids, sugars, peptides, organic or inorganic compounds, by the use of modified amino acids or the like. Protein modification techniques are illustrated in Ausubel et al. (eds) *Current Protocols in Molecular Biology*, John Wiley & Sons (1998).

Homologous sequences also means two sequences having a substantial percentage of sequence identity after alignment as determined by using sequence analysis programs for database searching and sequence alignment and comparison available, for example, from the Wisconsin Package Version 10.0, such as BLAST, FASTA, PILEUP, FINDPATTERNS or the like (GCG, Madison, WI). Public sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PhytoSeq (Incyte Pharmaceuticals, Palo Alto, CA) may be searched. Alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman (1981) *Adv. Appl. Math.* 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity method of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. U.S.A.* 85: 2444, by computerized implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence similarity. The comparison window may be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous positions. A description of the method is provided in Ausubel et al. (eds) (1999) *Current Protocols in Molecular Biology*, John Wiley & Sons.

Transcription factors that are homologs of the disclosed sequences will typically share at least 40% amino acid sequence identity. More closely related TFs may share at least 50%, 60%, 65%, 70%, 75% or 80% sequence identity with the disclosed sequences. Factors that are most closely related to the disclosed sequences share at least 85%, 90% or 95% sequence identity. At the nucleotide

level, the sequences will typically share at least 40% nucleotide sequence identity, preferably at least 50%, 60%, 70% or 80% sequence identity, and more preferably 85%, 90%, 95% or 97% sequence identity. The degeneracy of the genetic code enables major variations in the nucleotide sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein.

One way to identify whether two nucleic acid molecules are closely related is that the two molecules hybridize to each other under stringent conditions. Generally, stringent conditions are selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Conditions for nucleic acid hybridization and calculation of stringencies can be found in Sambrook et al. (1989) *Molecular Cloning. A Laboratory Manual*, Ed. 2, Cold Spring Harbor Laboratory Press, New York and Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes* Part I, Elsevier, New York. Nucleic acid molecules that hybridize under stringent conditions will typically hybridize to a probe based on either the entire cDNA or selected portions of the cDNA under wash conditions of 0.2x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C, for example 0.2 x SSC, 0.1% SDS at 65° C. For detecting less closely related homologs washes may be performed at 50° C.

For conventional hybridization the hybridization probe is conjugated with a detectable label such as a radioactive label, and the probe is preferably of at least 20 nucleotides in length. As is well known in the art, increasing the length of hybridization probes tends to give enhanced specificity. The labeled probe derived from the *Arabidopsis* nucleotide sequence may be hybridized to a plant cDNA or genomic library and the hybridization signal detected using means known in the art. The hybridizing colony or plaque (depending on the type of library used) is then purified and the cloned sequence contained in that colony or plaque isolated and characterized. Homologs may also be identified by PCR-based techniques, such as inverse PCR or RACE, using degenerate primers. See Ausubel et al. (eds) (1998) *Current Protocols in Molecular Biology*, John Wiley & Sons.

TF homologs may alternatively be obtained by immunoscreening an expression library. With the provision herein of the disclosed TF nucleic acid

sequences, the polypeptide may be expressed and purified in a heterologous expression system (e.g., *E. coli*) and used to raise antibodies (monoclonal or polyclonal) specific for the TF. Antibodies may also be raised against synthetic peptides derived from TF amino acid sequences. Methods of raising antibodies are well known in the art and are described in Harlow and Lane (1988) *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York. Such antibodies can then be used to screen an expression library produced from the plant from which it is desired to clone the TF homolog, using the methods described above. The selected cDNAs may be confirmed by sequencing and enzymatic activity.

3. Ectopic Expression of Transcription Factors

Any of the identified sequences may be incorporated into a cassette or vector for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described including those described in Weissbach and Weissbach, (1989) *Methods for Plant Molecular Biology*, Academic Press, and Gelvin et al., (1990) *Plant Molecular Biology Manual*, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella, L., et al., (1983) *Nature* 303: 209, Bevan, M., *Nucl. Acids Res.* (1984) 12: 8711-8721, Klee, H. J., (1985) *Bio/Technology* 3: 637-642, for dicotyledonous plants.

Alternatively, non-Ti vectors can be used to transfer the DNA into monocotyledonous plants and cells by using free DNA delivery techniques. Such methods may involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon carbide whiskers, and viruses. By using these methods transgenic plants such as wheat, rice (Christou, P., (1991) *Bio/Technology* 9: 957-962) and corn (Gordon-Kamm, W., (1990) *Plant Cell* 2: 603-618) can be produced. An immature embryo can also be a good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks, T. et al., (1993) *Plant Physiol.* 102: 1077-1084; Vasil, V., (1993) *Bio/Technology* 10: 667-674; Wan, Y. and Lemeaux, P., (1994) *Plant Physiol.* 104: 37-48, and for *Agrobacterium*-mediated DNA transfer (Ishida et al., (1996) *Nature Biotech.* 14: 745-750).

Typically, plant transformation vectors include one or more cloned plant coding sequence (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (e.g., a regulatory region controlling inducible or constitutive, environmentally-or developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

Examples of constitutive plant promoters which may be useful for expressing the TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-level expression in most plant tissues (see, e.g., Odel et al., (1985) *Nature* 313:810); the nopaline synthase promoter (An et al., (1988) *Plant Physiol.* 88:547); and the octopine synthase promoter (Fromm et al., (1989) *Plant Cell* 1: 977).

A variety of plant gene promoters that regulate gene expression in response to environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of the TF sequence in plants, as illustrated seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), fruit-specific promoters that are active during fruit ripening (such as the *dru 1* promoter (US Pat. No. 5,783,393), or the 2A11 promoter (US Pat. No. 4,943,674) and the tomato polygalacturonase promoter (Bird et al. (1988) *Plant Mol. Biol.* 11:651), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) *Plant Mol. Biol.* 37:977-988), flower-specific (Kaiser et al, (1995) *Plant Mol. Biol.* 28:231-243), pollen (Baerson et al. (1994) *Plant Mol. Biol.* 26:1947-1959), carpels (Ohl et al. (1990) *Plant Cell* 2:837-848), pollen and ovules (Baerson et al. (1993) *Plant Mol. Biol.* 22:255-267), auxin-inducible promoters (such as that described in van der Kop et al (1999) *Plant Mol. Biol.* 39:979-990 or Baumann et al. (1999) *Plant Cell* 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) *Plant Mol. Biol.* 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) *Plant Mol. Biol.* 38:1053-1060, Willmott et al. (1998) 38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley, et al. (1993) *Plant Mol. Biol.*

22: 13-23), light (e.g., the pea *rbcs*-3A promoter, Kuhlemeier et al., (1989) *Plant Cell* 1:471, and the maize *rbcs* promoter, Schaffner and Sheen, (1991) *Plant Cell* 3: 997); wounding (e.g., *wun1*, Siebertz et al., (1989) *Plant Cell* 1: 961); pathogen resistance, and chemicals such as methyl jasmonate or salicylic acid (Gatz et al., (1997) *Plant Mol. Biol.* 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at senescence (An and Amazon (1995) *Science* 270: 1986-1988); or late seed development (Odell et al. (1994) *Plant Physiol.* 106:447-458).

Plant expression vectors may also include RNA processing signals that may be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors may include additional regulatory sequences from the 3'-untranslated region of plant genes, e.g., a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region of potato or the octopine or nopaline synthase 3' terminator regions.

Finally, as noted above, plant expression vectors may also include dominant selectable marker genes to allow for the ready selection of transformants. Such genes include those encoding antibiotic resistance genes (e.g., resistance to hygromycin, kanamycin, bleomycin, G418, streptomycin or spectinomycin) and herbicide resistance genes (e.g., phosphinothricin acetyltransferase).

A reduction of TF expression in a transgenic plant to modify a plant trait may be obtained by introducing into plants antisense constructs based on the TF cDNA. For antisense suppression, the TF cDNA is arranged in reverse orientation relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length TF cDNA or gene, and need not be identical to the TF cDNA or a gene found in the plant type to be transformed. Generally, however, where the introduced sequence is of shorter length, a higher degree of homology to the native TF sequence will be needed for effective antisense suppression. Preferably, the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides. Transcription of an antisense construct as described results in the production of RNA molecules that are the reverse complement of mRNA molecules transcribed from the endogenous TF gene in the plant cell. Suppression of endogenous TF

gene expression can also be achieved using a ribozyme. Ribozymes are synthetic RNA molecules that possess highly specific endoribonuclease activity. The production and use of ribozymes are disclosed in U.S. Patent No. 4,987,071 to Cech and U.S. Patent No. 5,543,508 to Haselhoff. The inclusion of ribozyme sequences within antisense RNAs may be used to confer RNA cleaving activity on the antisense RNA, such that endogenous mRNA molecules that bind to the antisense RNA are cleaved, which in turn leads to an enhanced antisense inhibition of endogenous gene expression.

Vectors in which RNA encoded by the TF cDNA (or variants thereof) is over-expressed may also be used to obtain co-suppression of the endogenous TF gene in the manner described in U.S. Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire TF cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous TF gene. However, as with antisense suppression, the suppressive efficiency will be enhanced as (1) the introduced sequence is lengthened and (2) the sequence similarity between the introduced sequence and the endogenous TF gene is increased.

Vectors expressing an untranslatable form of the TF mRNA may also be used to suppress the expression of endogenous TF activity to modify a trait. Methods for producing such constructs are described in U.S. Patent No. 5,583,021 to Dougherty et al. Preferably, such constructs are made by introducing a premature stop codon into the TF gene. Alternatively, a plant trait may be modified by gene silencing using double-strand RNA (Sharp (1999) *Genes and Development* 13: 139-141).

Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a TF gene. Mutants containing a single mutation event at the desired gene may be crossed to generate homozygous plants for the mutation (Koncz et al. (1992) *Methods in Arabidopsis Research*. World Scientific).

A plant trait may also be modified by using the cre-lox system (for example, as described in US Pat. No. 5,658,772). A plant genome may be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the intervening DNA sequence between the two sites

is excised. If the lox sites are in the opposite orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention may also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of the endogenous gene by other means. For example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al., (1997) *Nature* 390 698-701, Kakimoto et al., (1996) *Science* 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the transcriptional machinery in a plant may be modified so as to increase transcription levels of a polynucleotide of the invention (See PCT Publications WO9606166 and WO 9853057 which describe the modification of the DNA binding specificity of zinc finger proteins by changing particular amino acids in the DNA binding motif).

4. Transgenic Plants with Modified TF Expression

Once an expression cassette comprising a polynucleotide encoding a TF gene of this invention has been constructed, standard techniques may be used to ectopically express the polynucleotide in a plant in order to modify a trait of the plant. The plant may be any higher plant, including gymnosperms, monocotyledonous and dicotyledonous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean, clover, etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcubitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.), *Solanaceae* (potato, tomato, tobacco, peppers, etc.), and various other crops. See protocols described in Ammirato et al. (1984) *Handbook of Plant Cell Culture –Crop Species*. Macmillan Publ. Co. Shimamoto et al. (1989) *Nature* 338:274-276; Fromm et al. (1990) *Bio/Technology* 8:833-839; and Vasil et al. (1990) *Bio/Technology* 8:429-434.

Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be transformed; those skilled in the art will recognize the suitability of particular methods for given plant types. Suitable

methods may include, but are not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumefaciens* mediated transformation. Transformation means introducing a nucleotide sequence in a plant in a manner to cause stable or transient expression of the sequence.

Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: U.S. Patent Nos. 5,571,706; 5,677,175; 5,510,471; 5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526; 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer antibiotic or herbicide resistance on the transformed plants, and selection of transformants can be accomplished by exposing the plants to appropriate concentrations of the antibiotic or herbicide.

After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modified trait may be any of those traits described above. Additionally, to confirm that the modified trait is due to changes in expression levels or activity of the polypeptide or polynucleotide of the invention may be determined by analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using immunoblots or Western blots or gel shift assays.

5. Other Utility of the Polypeptide and Polynucleotide Sequences

A transcription factor provided by the present invention may also be used to identify exogenous or endogenous molecules that may affect expression of the transcription factors and may affect any of the traits/phenotypes described herein. These molecules may include organic or inorganic compounds.

For example, the method may entail first placing the molecule in contact with a plant or plant cell. The molecule may be introduced by topical administration, such as spraying or soaking of a plant, and then the molecule's

effect on the expression or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide may be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding polynucleotide sequence may be detected by use of microarrays, Northern or any other technique for monitoring changes in mRNA expression. These techniques are exemplified in Ausubel et al. (eds) *Current Protocols in Molecular Biology*, John Wiley & Sons (1998). Such changes in the expression levels may be correlated with modified plant traits and thus identified molecules may be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

The transcription factors may also be employed to identify promoter sequences with which they may interact. After identifying a promoter sequence, interactions between the transcription factor and the promoter sequence may be modified by changing specific nucleotides in the promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA binding sites are identified by gel shift assays. After identifying the promoter regions, the promoter region sequences may be employed in double-stranded DNA arrays to identify molecules that affect the interactions of the TFs with their promoters (Bulyk et al. (1999) *Nature Biotechnology* 17:573-577).

The identified transcription factors are also useful to identify proteins that modify the activity of the transcription factor. Such modification may occur by covalent modification, such as by phosphorylation, or by protein-protein (homo or heteropolymer) interactions. Any method suitable for detecting protein-protein interactions may be employed. Among the methods that may be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

The two-hybrid system detects protein interactions in vivo and is described in Chien, et al., (1991), *Proc. Natl. Acad. Sci. USA*, 88, 9578-9582 and is commercially available from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been

recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library plasmids responsible for reporter gene expression are isolated and sequenced to identify the proteins encoded by the library plasmids. After identifying proteins that interact with the transcription factors, assays for compounds that interfere with the TF protein-protein interactions may be preformed.

The following examples are intended to illustrate but not limit the present invention.

Example I. Full Length Gene Identification and Cloning

Putative transcription factor sequences (genomic or ESTs) related to known transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of -4 or -5 or lower, depending on the length of the query sequence. Putative transcription factor sequence hits were then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription factors.

As an example, members of the MYB transcription factor family were identified as such if they had one of the following sequence strings:

a) LRWXXNYLRPXKXRGXFXEEXIXLHXXGNXWSXIXAXLPXGXR,

b) LRWXXNYLRPXXKRGXFXEEXIXXXLHXXXGNXWSXIA,

c) KGXWXXEEDXXL, or

d) LRWXXNYLRPXXXXGXXXXXEXXXXXLHXXXGNXWSXIXAXLPGR

Alternatively, *Arabidopsis thaliana* cDNA libraries derived from different tissues or treatments, or genomic libraries were screened to identify novel

members of a transcription family using a low stringency hybridization approach. Probes were synthesized using gene specific primers in a standard PCR reaction (annealing temperature 60° C) and labeled with ³²P dCTP using the High Prime DNA Labeling Kit (Boehringer Mannheim). Purified radiolabelled probes were added to filters immersed in Church hybridization medium (0.5 M NaPO₄ pH 7.0, 7% SDS, 1 % w/v bovine serum albumin) and hybridized overnight at 60 °C with shaking. Filters were washed two times for 45 to 60 minutes with 1xSSC, 1% SDS at 60° C.

As an example, the following GiD Nos. may be screened with the primers found in Table 3.

Table 3

GiD No.	Forward primer	Reverse Primer
G1035	ACTTTGGGTCCTGCGTCTTAATC ATAGT	ATTACAGTTTTACCCCTGCTGCG ATGA
G663	GAAGCCACAATAACCCCTATTTC CTC	TACGAAAGAAAAAGCCACCCACA ATCT
G867	TGGAATCGAGTAGCGTTGATGA GAGT	AGAAGAAGAGTTGTTACGAGGC GTGA
G1334	ATGCAAACTGAGGAGCTTTTGT CGCCA	AGGCAGAGTTTCTTACAACACAC ACT
G921	ATCTCTCTCAACTTCTCTCTCA GCT	AGCTGCTGCTAAAGCTGCTGTAA AGT

To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed using the Marathon™ cDNA amplification kit (Clontech, Palo Alto, CA). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to generate double stranded cDNA, blunting cDNA ends, followed by ligation of the Marathon™ Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA. Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Nested primers, rather than single primers, were used to increase PCR specificity. Using 5' and 3' RACE reactions, 5' and 3' RACE fragments were obtained.

sequenced and cloned. The process may be repeated until 5' and 3' ends of the full-length gene were identified. Then the full-length cDNA was generated by PCR using primers specific to 5' and 3' ends of the gene by end-to-end PCR.

5 **Example IIa Pathogen Resistance Genes**

The sequences shown in Table 4 were identified as being induced during exposure to pathogens.

RT-PCR experiments were performed to identify those genes induced after exposure to biotrophic fungal pathogens, such as *Erysiphe orontii*, necrotrophic
10 fungal pathogens, such as *Fusarium oxysporum*, and salicylic acid which is involved in a nonspecific resistance response in *Arabidopsis thaliana*. The gene expression patterns from ground plant tissue were investigated.

Fusarium oxysporum isolates cause vascular wilts and damping off of various annual vegetables, perennials and weeds (Mauch-Mani and Slusarenko
15 (1994) Molecular Plant-Microbe Interactions 7: 378-383). For *Fusarium oxysporum* experiments, plants grown on petri dishes were sprayed with a fresh spore suspension of *F. oxysporum*. The spore suspension was prepared as follows: A plug of fungal hyphae from a plate culture was placed on a fresh potato dextrose agar plate and allowed to spread for one week. 5 ml sterile water was then added
20 to the plate, swirled, and pipetted into 50 ml Armstrong Fusarium medium. Spores were grown overnight in Fusarium medium and then sprayed onto plants using a Preval paint sprayer. Plant tissue was harvested and frozen in liquid nitrogen 48 hours post infection

Erysiphe orontii is a causal agent of powdery mildew. For *Erysiphe orontii*
25 experiments, plants were grown approximately 4 weeks in a greenhouse under 12 hour light (20 C, ~30% relative humidity (rh)). Individual leaves were infected with *E. orontii* spores from infected plants using a camel's hair brush, and the plants were transferred to a Percival growth chamber (20 C, 80% rh.). Plant tissue was harvested and frozen in liquid nitrogen 7 days post infection.

For salicylic acid experiments, 15 day old seedlings grown on petri dishes
30 were transferred to plates containing 0.5 mM salicylic acid (SA). After 72 hours, leaves were harvested and frozen in liquid nitrogen.

Reverse transcriptase PCR was done using gene specific primers within the coding region for each sequence identified. The primers were designed near the 3' region of each coding sequence initially identified.

Total RNA from these tissues were isolated using the CTAB extraction protocol. Once extracted total RNA was normalized in concentration across all the tissue types to ensure that the PCR reaction for each tissue received the same amount of cDNA template using the 28S band as reference. Poly A+ was purified using a modified protocol from the Qiagen Oligotex kit batch protocol. cDNA was synthesized using standard protocols. After the first strand cDNA synthesis, primers for Actin 2 were used to normalize the concentration of cDNA across the tissue types. Actin 2 is found to be constitutively expressed in fairly equal levels across the tissue types we are investigating.

For RT PCR, cDNA template was mixed with corresponding primers and Taq polymerase. Each reaction consisted of 0.2 ul cDNA template, 2ul 10X Tricine buffer, 2 ul 10X Tricine buffer and 16.8 ul water, 0.05ul Primer 1, 0.05 ul, Primer 2, 0.3 ul Taq polymerase and 8.6 ul water.

The 96 well plate was covered with microfilm and set in the Thermocycler to start the following reaction cycle. Step1 93° C for 3 mins, Step 2 93° C for 30 sec, Step 3 65° C for 1 min, Step 4 72° C for 2 mins,. Steps 2, 3 and 4 were repeated for 28 cycles, Step 5 72° C for 5 mins and Step 6 4° C. The PCR plate was placed back in the thermocycler to amplify more products at 8 more cycles to identify genes that have very low expression. The reaction cycle was as follows: Step 2 93° C for 30 sec, Step 3 65° C for 1 min, and Step 4 72° C for 2 ins, repeated for 8 cycles, and Step 4 4° C.

8ul of PCR product and 1.5 ul of loading dye were loaded on a 1.2% agarose gel for analysis after 28 cycles and 36 cycles. Expression levels of specific transcripts were considered low if they were only detectable after 36 cycles of PCR. Expression levels were considered medium or high depending on the levels of transcript compared with observed transcript levels for actin2.

The transcript levels were upregulated in three repeat experiments whereas in control experiments lower transcript levels were detectable.

Table 4

SEQ ID No.	GID No.	Expression Induced by:
SEQ ID No. 43	G663 (MYB)	<i>Fusarium</i> , SA
SEQ ID No. 17	G867 (AP2)	<i>Erysyphe</i>
SEQ ID No. 83	G920 (WRKY)	<i>Erysyphe</i> , SA
SEQ ID No. 85	G921 (WRKY)	<i>Fusarium</i> , <i>Erysyphe</i> , SA
SEQ ID No. 129	G1334 (CAAT)	SA
SEQ ID No. 87	G986 (WRKY)	<i>Erysyphe</i>
SEQ ID No. 91	G1043 (WRKY)	<i>Erysyphe</i>
SEQ ID No. 1061	G1048 (bZIP)	<i>Erysyphe</i>

Example IIb. Environmental Stress Genes

The sequences shown in Table 5 were identified as being induced during exposure to an environmental stress.

RT-PCR experiments using treated rosette leaf tissue were performed as described above to identify those genes induced after exposure of the plants or seedlings to chilling stress (6 hour exposure to 4° C), heat stress (6 hour exposure to 37° C), high salt stress (6 hour exposure to 200 mM NaCl), drought stress (168 hours after removing water from trays), osmotic stress (6 hour exposure to 3 M mannitol), hormones (6 hours after spraying plants with 1 uM indole acetic acid (2,4-D) or 50 uM abscisic acid (ABA)). The gene expression patterns from ground plant leaf tissue was investigated as described above.

The transcript levels were upregulated in seven experiments whereas in control experiments lower levels were observed.

Table 5

SEQ ID No.	GID No.	Expression Induced by:
SEQ ID No. 9	G10 (AP2)	2,4-D; Cold
SEQ ID No. 43	G663 (MYB)	2,4-D; ABA; Cold; Drought; Osmotic
SEQ ID No. 17	G867 (AP2)	2,4-D; Cold
SEQ ID No. 85	G921 (WRKY)	All, but salt
SEQ ID No. 27	G975 (AP2)	Cold; Drought
SEQ ID No. 65	G1328 (MYB)	ABA; Osmotic

SEQ ID No. 129	G1334 (CAAT)	Heat; Drought
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Example IIc. Seed or Root Active Genes

The sequences in Table 6 were expressed at higher levels in seeds or roots compared with other plant tissue.

For preparation of seed tissue the following protocol was used. About 10-20g of frozen siliques were poured into a chilled pestle. The frozen siliques were repeatedly tapped and occasionally very lightly ground with a pestle. After several minutes of the tapping procedure, the broken, frozen siliques were poured through a pre-chilled fine mesh sieve made of metal, into another chilled mortar containing a small amount of liquid nitrogen assuring that the broken material was completely frozen but free of liquid nitrogen before beginning the pouring and sifting process. After the sieve has been filled with the broken material, lightly tap the edge of the sieve to cause the immature seeds to fall through the mesh into the liquid nitrogen (at this point, small pieces of contaminating tissue will also pass through the sieve). This process was repeated until almost all of the siliques were broken open, and very few attached immature seeds were visible. The harvested immature seeds can then be filtered several times through the sieve to further remove contaminating tissue. The immature seeds were stored at -80° C until further use once the seeds contained less than 1-2% contaminating tissue.

RT-PCR experiments were performed as described above.

Table 6

SEQ ID No.	GID No.	Activity
SEQ ID No. 9	G10 (AP2)	Root
SEQ ID No. 17	G867 (AP2)	Root
SEQ ID No. 3	G5 (AP2)	Root
SEQ ID No. 35	G993 (AP2)	Root
SEQ ID No. 125	G699 (HB)	Root
SEQ ID No. 93	G1091 (WRKY)	Root
SEQ ID No. 57	G932 (MYB)	Seed
SEQ ID No. 67	G858 (MADS)	Seed

SEQ ID No. 21	G872 (AP2)	Seed
SEQ ID No. 97	G838 (AKR)	Seed
SEQ ID No. 43	G663 (MYB)	Seed
SEQ ID No. 159	G1035 (bZIP)	Seed
SEQ ID No. 135	G462 (IAA/AUX)	Shoots

Example IV. Construction of Expression Vectors

The sequence was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. The expression vector was pMEN001, which is derived from pBin19 (Bevan M (1984) *Nucleic Acids Research* 12:8711-8720). To clone the sequence into the vector, both pMEN001 and the genomic sequence clone were digested separately with Sall and XbaI restriction enzymes at 37° C for 2 hours. The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized by ethidium bromide staining. The DNA fragments containing the sequence and the linearized plasmid were excised and purified by using a Qiaquick gel extraction kit (Qiagen, CA). The fragments of interest were ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, MA) were carried out at 16° C for 16 hours. The ligated DNAs were transformed into competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l kanamycin (Sigma).

Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l kanamycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini Prep kits (Qiagen, CA).

Example V. Transformation of *Agrobacterium* with the Expression Vector

After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of *Agrobacterium tumefaciens* cells for transformation were made as described by Nagel et al. *FEMS Microbiol Letts* 67: 325-328 (1990). *Agrobacterium* strain GV3101 was grown in 250 ml LB medium (Sigma) overnight at 28°C with shaking until an absorbance (A_{600}) of 0.5 – 1.0 was reached. Cells were harvested by centrifugation at 4,000 x g for 15 min at 4° C. Cells were

then resuspended in 250 μ l chilled buffer (1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were centrifuged again as described above and resuspended in 125 μ l chilled buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 μ l and 750 μ l, respectively. Resuspended cells were then distributed into 40 μ l aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

Agrobacterium cells were transformed with plasmids prepared as described above following the protocol described by Nagel et al. *FEMS Microbiol Letts* 67: 325-328 (1990). For each DNA construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 μ l of *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 μ F and 200 μ F using a Gene Pulser II apparatus (Bio-Rad). After electroporation, cells were immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28° C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100 μ g/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28° C. Single colonies were then picked and inoculated in fresh medium. The presence of the plasmid construct was verified by PCR amplification and sequence analysis.

Example VI. Transformation of *Arabidopsis* Plants with *Agrobacterium tumefaciens* with Expression Vector

After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l kanamycin were inoculated with the colonies and grown at 28° C with shaking for 2 days until an absorbance (A_{600}) of > 2.0 is reached. Cells were then harvested by centrifugation at $4,000 \times g$ for 10 min, and resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044 μ M benzylamino purine (Sigma), 200 μ l/L Silwet L-77 (Lehle Seeds) until an absorbance (A_{600}) of 0.8 was reached.

Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium

(Hummert International) covered with fiberglass mesh (18 mm X 16 mm). Plants were grown under continuous illumination (50-75 $\mu\text{E}/\text{m}^2/\text{sec}$) at 22-23° C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of multiple secondary bolts. After flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium* infiltration medium as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The immersion procedure was repeated one week later, for a total of two immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

Example VII. Identification of Arabidopsis Primary Transformants

Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and sterile H_2O and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After removal of the second wash solution, a solution containing 0.1% (v/v) Triton X-100 and 70% ethanol (Equistar) was added to the seeds and the suspension was shaken for 5 min. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30% (v/v) bleach (Clorox) was added to the seeds, and the suspension was shaken for 10 min. After removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled H_2O . The seeds were stored in the last wash water at 4° C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH adjusted to 5.7 with 1M KOH), 1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l kanamycin). Seeds were germinated under continuous illumination (50-75 $\mu\text{E}/\text{m}^2/\text{sec}$) at 22-23° C. After 7-10 days of growth under these conditions, kanamycin resistant primary transformants (T_1 generation) were visible and obtained. These seedlings were transferred first to fresh selection plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX potting medium).

Primary transformants are crossed and progeny seeds (T_2) collected; kanamycin resistant seedlings are selected and analyzed as described above.

Example VIIIa. Pathogen Resistance or Tolerance in Transgenic Plants

Pathogen resistance or pathogen tolerance in a transgenic *Arabidopsis* plant is compared with that of a wild type plant.

Two week old *Arabidopsis* seedlings are inoculated with *Fusarium* by spraying with a spore suspension (2×10^6 conidia per millimeter) and incubated under high humidity. Plants are then scored macroscopically for disease symptoms or microscopically for fungal growth or using microarrays for the induction of resistance associated genes (such as the defensin genes) to detect resistance or tolerance of the plant tissue. A wild type plant should show the first signs of damage (gradual yellowing of leaves, damping off of seedlings or growth of fungal mycelium) after four days from inoculation. Wild type resistant ecotypes should show some damage after 2 weeks. Transgenic plants which are pathogen tolerant should show the initial symptoms between 4 days and 2 weeks. Transgenic plants (from a nonresistant phenotype) which are pathogen resistant should show initial signs of damage, if any, after 2 weeks.

Erysiphe inoculations are done by tapping conidia from 1 to 2 heavily infected leaves onto the mesh cover of a settling tower, brushing the mesh with a camel's hair paint brush to break up the conidial chains, and letting the conidia settle for 10 minutes. Plants are 4 to 4.5 weeks old at the time of inoculation. Spores are obtained from 10 to 14 day old *Erysiphe* cultures. The mesh has a pore size of 95 microns; the settling towers are 28" high, and wide enough to fit over a box of plants (6"x6" or 6"x8"). Symptoms are evaluated 7–21 days post-inoculation. Typically, within the first twenty-four hours, the spores differentiate into several fungal structures including the haustorium that invaginates a host's epidermal plasma membrane. Formation of aerial mycelium and sporulation represent late differentiation events between 4 and 7 days post inoculation (Freilaldenhoven et al. (1994) *Plant Cell* 6: 983-994). Events associated with resistance or tolerance to the pathogen includes: the induction of pathogen resistance related genes (R genes), the activation of cell death in the attacked epidermal cells (hypersensitive response), the induction of certain chemicals, such as phytoalexins, and the lignification that occurs at attempted penetration sites.

Assays are performed to observe these events. Transgenic plants are identified that induce R genes, activate cell death, induce chemicals or increase lignification sooner or to a greater extent than wild type plants when exposed to A pathogen.

These transgenic plants may be more resistant to biotrophic or necrotrophic pathogens such as a fungus, bacterium, mollicute, virus, nematode, a parasitic higher plant or the like and associated diseases. In particular, pathogens such as *Fusarium oxysporum*, *Erysiphe orontii* and other powdery mildews, *Sclerotinia spp.*, soil-borne oomycetes, foliar oomycetes, *Botrytis spp.*, *Rhizoctonia spp.*, *Verticillium dahliae/albo-atrum*, *Alternaria spp.*, rusts, *Mycosphaerella spp.*, *Fusarium solani*, or the like. The diseases include fungal diseases such as rusts, smuts, wilts, yellows, root rot, leaf drop, ergot, leaf blight of potato, brown spot of rice, leaf blight, late blight, powdery mildew, downy mildew, and the like; viral diseases such as sugarcane mosaic, cassava mosaic, sugar beet yellows, plum pox, barley yellow dwarf, tomato yellow leaf curl, tomato spotted wilt virus, and the like; bacterial diseases such as citrus canker, bacterial leaf blight, bacterial wilt, soft rot of vegetables, and the like; nematode diseases such as root knot, sugar beet cyst nematode or the like.

Example VIIIb. Seed or Root Trait Modification

Transgenic plants are identified that ectopically express those transcription factors that are active in seed or roots. These plants may have improved seed germination characteristics; shelf-life; seed drydown characteristics; size; stress responses, such as to heat, chilling, freezing, high salt or osmotic shock; protein, oil or starch content; other nutritional content, such as vitamins, minerals, flavonoids, phytosterols or phytic acid; seedling vigor; insect resistance, or seed coat quality. The same or other plants may have improved root characteristics such as root hair number, stress responses, in particular to drought, root length, pest resistance, absorption of nutrients, such as nitrogen and phosphorus containing compounds, or the like.

Example VIIIc. Other Trait Modifications

Transgenic plants overexpressing the identified TF genes are shown with observed trait modifications in Table 7.

Table 7

SEQ ID No.	GID No. (Family)	Phenotype
SEQ ID No. 151	G629 (bZIP)	Tolerant to potassium deficiency
SEQ ID No. 153	G630 (bZIP)	Increased insoluble sugar
SEQ ID No. 123	G399 (HB)	More sensitive to high osmotic conditions, more beta-carotene and lutein, oil content modified
SEQ ID No. 125	G699 (HB)	More tolerant to high osmotic conditions
SEQ ID No. 127	G964 (HB)	Modifies normal responses to temperature, better germination in heat, early flowering
SEQ ID No. 43	G663 (MYB)	High pigment, increased fatty acid content, growth regulator, modified sensitivity to ethylene, pathogen resistance
SEQ ID No. 45	G664 (MYB)	More rapid growth and germination, modified responses to temperature, tolerant to potassium deficiency
SEQ ID No. 47	G672 (MYB)	Tolerant to high salt
SEQ ID No. 117	G911 (Z)	Tolerant to potassium deficiency
SEQ ID No. 19	G869 (AP2)	Modified flowering response
SEQ ID No. 37	G1020 (AP2)	Modified flowering response
SEQ ID No. 157	G1034 (bZIP)	Modified ethylene sensitivity
SEQ ID No. 137	G782 (HLH/MYC)	Tolerance to increased osmotic pressure
SEQ ID No. 139	G783 (HLH/MYC)	Tolerance to increased osmotic pressure
SEQ ID No. 105	G751 (Z)	Modified sensitivity to ethylene

Those transgenic plants with trait modifications associated with germination, flowering time are useful for reducing breeding time for crops, allowing long generation time plants such as trees to propagate faster, and reducing generation time for crops to allow more harvests per growing season. Those

transgenic plants with altered flowering times may also be employed for delaying flowering to allow more vegetative grow to increase yield. e.g. sugarbeet, regulating the vernalization process to allow growth of high yield winter crops in warmer regions, preventing vegetative crops from flowering hence reducing the possibility of pollen escape for genetically modified organisms, altering the architecture of plants for better vegetative growth or for ornamental plants, synchronizing blooming time using a inducible system, or reducing frost damage to blossom by delaying the flower time and induce later.

Those transgenic plants exhibiting a modified uptake of micronutrients are useful for growing plants in areas where such micronutrients are deficient or to minimize the use of fertilizers. Those transgenic plants able to withstand higher osmotic pressure or high salt are useful for growth in more arid conditions than normal for the wild type plant and may be more able to survive drought conditions. Those transgenic plants exhibiting a modified carotene or oil content are useful for increasing the nutritional value of the plant.

Example IX. Transformation of Cereal Plants with the Expression Vector

A cereal plant, such as corn, wheat, rice, sorghum or barley, can also be transformed with the plasmid vectors containing the sequence and constitutive or inducible promoters to modify a trait. In these cases, a cloning vector, pMEN020, is modified to replace the NptII coding region with the BAR gene of *Streptomyces hygroscopicus* that confers resistance to phosphinothricin. The KpnI and BglII sites of the Bar gene are removed by site-directed mutagenesis with silent codon changes.

Plasmids according to the present invention may be transformed into corn embryogenic cells derived from immature scutellar tissue by using microprojectile bombardment, with the A188XB73 genotype as the preferred genotype (Fromm et al., *Bio/Technology* 8: 833-839 (1990); Gordon-Kamm et al., *Plant Cell* 2: 603-618 (1990)). After microprojectile bombardment the tissues are selected on phosphinothricin to identify the transgenic embryogenic cells (Gordon-Kamm et al., *Plant Cell* 2: 603-618 (1990)). Transgenic plants are regenerated by standard corn regeneration techniques (Fromm, et al., *Bio/Technology* 8: 833-839 (1990); Gordon-Kamm et al., *Plant Cell* 2: 603-618 (1990)).

Example X. Identification of Homologous Sequences

Homologs from the same plant, different plant species or other organisms were identified using database sequence search tools, such as the Basic Local Alignment Search Tool (BLAST) (Altschul et al. (1990) *J. Mol. Biol.* 215:403-410; and Altschul et al. (1997) *Nucl. Acid Res.* 25: 3389-3402). The tblastn or blastn sequence analysis programs were employed using the BLOSUM-62 scoring matrix (Henikoff, S. and Henikoff, J. G. (1992) *Proc. Natl. Acad. Sci. USA* 89: 10915-10919). The output of a BLAST report provides a score that takes into account the alignment of similar or identical residues and any gaps needed in order to align the sequences. The scoring matrix assigns a score for aligning any possible pair of sequences. The P values reflect how many times one expects to see a score occur by chance. Higher scores are preferred and a low threshold P value threshold is preferred. These are the sequence identity criteria. The tblastn sequence analysis program was used to query a polypeptide sequence against six-way translations of sequences in a nucleotide database. Hits with a P value less than -25, preferably less than -70, and more preferably less than -100, were identified as homologous sequences. The blastn sequence analysis program was used to query a nucleotide sequence against a nucleotide sequence database. In this case too, higher scores were preferred and a preferred threshold P value was less than -13, preferably less than -50, and more preferably less than -100.

Alternatively, a fragment of a sequence from Table 1 is ³²P-radiolabeled by random priming (Sambrook et al., (1989) *Molecular Cloning. A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press, New York) and used to screen a plant genomic library. As an example, total plant DNA from *Arabidopsis thaliana*, *Nicotiana tabacum*, *Lycopersicon pimpinellifolium*, *Prunus avium*, *Prunus cerasus*, *Cucumis sativus*, or *Oryza sativa* are isolated according to Stockinger al (Stockinger, E. J., et al., (1996), *J. Heredity*, 87:214-218). Approximately 2 to 10 µg of each DNA sample are restriction digested, transferred to nylon membrane (Micron Separations, Westboro, MA) and hybridized. Hybridization conditions are: 42° C in 50% formamide, 5X SSC, 20 mM phosphate buffer 1X Denhardt's, 10% dextran sulfate, and 100µg/ml herring sperm DNA. Four low stringency washes at RT in 2X SSC, 0.05% sodium sarcosyl and 0.02% sodium pyrophosphate are performed prior to high stringency washes at 55° C in 0.2X

SSC, 0.05% sodium sarcosyl and 0.01% sodium pyrophosphate. High stringency washes are performed until no counts are detected in the washout according to Walling et al. (Walling, L. L., et al., (1988) Nucl. Acids Res. 16:10477-10492).

5 All references (publications and patents) are incorporated herein by reference in their entirety for all purposes.

Although the invention has been described with reference to the embodiments and examples above, it should be understood that various modifications can be made without departing from the spirit of the invention.
10 Accordingly, the invention is limited only by the following claims.

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We Claim:

- 5 1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from the group consisting of SEQ ID Nos. 2N-1, where N= 1-85; (b) a nucleotide sequence encoding a polypeptide comprising a sequence selected from the group consisting of SEQ ID Nos. 2N-1, where N= 1-85; including substitutions, deletions or insertions; (c) a nucleotide sequence encoding a fragment from a polypeptide of (a) or (b); (d) a nucleotide sequence comprising a sequence selected from the group consisting of SEQ ID Nos. 2N-1, where N= 1-85; (e) a nucleotide sequence having at least 40% identity with a nucleotide sequence of (a) or (b); (f) a nucleotide sequence having at least 60% identity with a nucleotide sequence of (c); (g) a nucleotide sequence comprising at least 15 consecutive nucleotides of SEQ ID Nos. 2N-1, where N=1-85; and (h) a nucleotide sequence that hybridizes to a sequence encoding a polypeptide of (a), (b) or (c) under stringent conditions.
- 10
- 15
- 20 2. The isolated polynucleotide of claim 1, further comprising a constitutive promoter operably linked to said nucleotide sequence
- 25 3. The isolated polynucleotide of claim 1, further comprising an inducible promoter operably linked to said nucleotide sequence.
- 30 4. The isolated polynucleotide of claim 1, further comprising a tissue-active promoter operably linked to said nucleotide sequence.
5. An expression vector comprising an isolated polynucleotide of claim 1.
6. A host cell comprising an expression vector of claim 5.

7. A transgenic plant comprising an isolated polynucleotide of claim 1.

8. A transgenic plant ectopically expressing an isolated polynucleotide of claim 1.

5

9. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of: (a) a sequence selected from SEQ ID Nos. 2(N), where N= 1-85; (b) a sequence selected from SEQ ID Nos. 2(N), where N= 1-85; including substitutions, deletions or insertions; (c) a sequence from a fragment from a polypeptide of (a) or (b); (d) a sequence having at least 40% identity with a sequence of (a) or (b); and (e) a sequence having at least 60% identity with a sequence of (a) or (b).

10

10. A transgenic plant ectopically expressing an isolated polypeptide of claim 9.

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11. A method for screening a molecule to identify a molecule that modifies a plant trait, said method comprising (a) placing the molecule in contact with the plant; and (b) monitoring the effect of the molecule on the expression or activity of a polypeptide of claim 9 or the expression of a polynucleotide of claim 1.

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12. A method for producing a transgenic plant having a modified trait, said method comprising ectopically expressing the isolated polynucleotide of claim 1 and selecting a plant with the modified trait.

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13. A method for identifying a sequence homologous to the polynucleotide of claim 1, said method comprising (a) providing a database sequence; (b) aligning and comparing the sequence of the polynucleotide of claim 1 with the database sequence to determine whether the database sequence meets sequence identity criteria relative to the polynucleotide of claim 1; and (c) selecting a database sequence that meets the sequence identity criteria.

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14. A polynucleotide sequence identified by the method of claim 13.

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ABSTRACT OF THE INVENTION

Compositions and methods are provided for modifying a trait of a plant. Isolated polynucleotide and polypeptide sequences are provided, along with an expression vector comprising the isolated polynucleotide, a host cell comprising the isolated polynucleotide, and a transgenic plant comprising the isolated polynucleotide. Also provided is a method for producing a transgenic plant, a method for screening for a compound that may modify the trait and a method for identifying other homologous polynucleotide and polypeptide sequences.

5

10

As a below-named inventor, I hereby declare that:

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

the specification of which is attached hereto.

I acknowledge the duty to disclose all information which is material to patentability as defined in Title 37, Code of Federal Regulations, § 1.56(a) which states in relevant part: "Each individual associated with the filing and prosecution of a patent application has a duty of candor and good faith in dealing with the Office, which includes a duty to disclose to the Office all information known to that individual to be material to patentability as defined in this section. The duty to disclose all information known to be material to patentability is deemed to be satisfied if all information known to be material to patentability of any claim issued in a patent was cited by the Office or submitted to the Office in the manner prescribed by §§ 1.97(b)-(d) and 1.98.

I hereby claim foreign priority benefits under Title 35 United States Code, § 119(a)-(d) or 365(a)-(b) of any foreign applications for patent or inventor's certificate as indicated below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

I hereby claim the benefit of priority under Title 35 United States Code, § 119(e) of any United States provisional application(s) listed below:

Provisional Serial Nos. 60/101,349
60/103,312
60/108,734
60/113,409

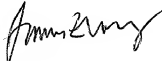
Filing Dates: 9/22/98
10/6/98
11/17/98
12/22/98

I hereby claim the benefit under Title 35 United States Code, § 120 of any United States applications listed below and, insofar as this is a continuation-in-part application filed under the conditions set forth in 35 United States Code, § 120, which discloses and claims subject matter in addition to the prior copending application(s) listed below, I acknowledge the duty to disclose to the United States Patent Office all information known to be material to patentability as defined in Title 37 Code of Federal Regulations, § 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application:

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Title 18, United States Code, §1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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00369519 081399

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Title 18, United States Code, §1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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X a copy of an Assignment attached hereto, which Assignment has been (or is herewith) forwarded to the Patent and Trademark Office for recording; or

- the Assignment recorded on _____ at reel __, frames __ - __.

Pursuant to 37 C.F.R. § 3.73(b) the undersigned Assignee hereby states that evidentiary documents have been reviewed and hereby certifies that, to the best of ASSIGNEE's knowledge and belief, title is in the identified ASSIGNEE.

Direct all telephone calls to Karen J. Guerrero (510) 264-0280 ext. 125.

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Name: *Michael Fromm*

Name:
Michael Fromm

Title:
President and CEO

Date: *9/8/99*

2025 RELEASE UNDER E.O. 14176

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: MBI-0003

In re patent application of

Heard, Jacqueline et al.

Serial No. Unassigned

Filed: Concurrently Herewith

For: PLANT GENE SEQUENCES I

STATEMENT TO SUPPORT FILING AND SUBMISSION IN
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(q), does not include new matter;

2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and

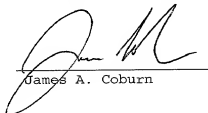
3. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United

Serial No. Unassigned

States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

Aug. 30, 1999
Date


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60210-454063

gat ttc ata cct ccg ccg agg tcc ctc cgc gtc act aac gag ttt atc 161
Asp Phe Ile Pro Pro Pro Arg Ser Leu Arg Val Thr Asn Glu Phe Ile
10 15 20

tgg ccg gat ctg aaa aac aaa gtg aaa gct tca aag aag aga tcg aat	209
Trp Pro Asp Leu Lys Asn Lys Val Lys Ala Ser Lys Lys Arg Ser Asn	
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aag cga tcc gat ttc ttc gat ctt gac gat gat ttc gaa gct gat ttc	257
Lys Arg Ser Asp Phe Phe Asp Leu Asp Asp Asp Phe Glu Ala Asp Phe	
45 50 55	
caa ggg ttt aag gat gac tcg gct ttt gac tgc gaa gac gat gat gat	305
Gln Gly Phe Lys Asp Asp Ser Ala Phe Asp Cys Glu Asp Asp Asp Asp	
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Val Phe Val Asn Val Lys Pro Phe Val Phe Thr Ala Thr Lys Pro	
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Val Ala Ser Ala Phe Val Ser Thr Val Gly Ser Ala Tyr Ala Lys Lys	
90 95 100	
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Thr Val Glu Ser Ala Glu Glu Ala Glu Lys Ser Ser Lys Arg Lys Arg	
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aag aat car tac cga ggg att agg cag cgt cct tgg gga aaa tgg gct	497
Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala	
125 130 135	
gcg gag atc cgt gat ccg aga aaa ggc tcc cga gaa tgg ctt gga aca	545
Ala Glu Ile Arg Asp Pro Arg Lys Gly Ser Arg Glu Trp Leu Gly Thr	
140 145 150	
ttc gac act gct gag gaa gca gca aga gct tat gat gct gca gca cgc	593
Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Arg	
155 160 165	
aga atc cgt ggc acg aaa gct aag gtg aat ttt ccc gag gag aag aac	641
Arg Ile Arg Gly Thr Lys Ala Lys Val Asn Phe Pro Glu Glu Lys Asn	
170 175 180	
cct agc gtc gta tcc cag aaa cgt cct agt gct aag act aat aat ctt	689
Pro Ser Val Val Ser Gln Lys Arg Pro Ser Ala Lys Thr Asn Asn Leu	
185 190 195 200	
cag aaa tca gtg gct aaa cca aac aaa agc gta act ttg gtt cag cag	737
Gln Lys Ser Val Ala Lys Pro Asn Lys Ser Val Thr Leu Val Gln Gln	
205 210 215	
cca aca cat ctg agt cag cag tac tgc aac aac tcc ttt gac aac tct	785
Pro Thr His Leu Ser Gln Gln Tyr Cys Asn Asn Ser Phe Asp Asn Ser	
220 225 230	
ttt ggt gat atg agt ttc atg gaa gag aag cct cag atg tac aac aat	833
Phe Gly Asp Met Ser Phe Met Glu Glu Lys Pro Gln Met Tyr Asn Asn	
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 Gln Tyr Phe Ser Ser Asp Gln Gly Ser Asn Ser Phe Asp Cys Ser Met
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 Phe Gly Trp Ser Asp His Gly Pro Lys Thr Pro Glu Ile Ser Ser Met
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 Leu Val Asn Asn Asn Glu Ala Ser Phe Val Glu Glu Thr Asn Ala Ala
 300 305 310
 aag aag ctc aaa cca aac tct gat gag tca gac gat ctg atg gca tac 1073
 Lys Lys Leu Lys Pro Asn Ser Asp Glu Ser Asp Asp Leu Met Ala Tyr
 315 320 325
 ctt gac aac gcc ttg tgg gac acc cca cta gaa gtg gaa gcc atg ctt 1121
 Leu Asp Asn Ala Leu Trp Asp Thr Pro Leu Glu Val Glu Ala Met Leu
 330 335 340
 ggc gca gat gct ggt gct gtg act cag gaa gag gaa aac cca gtg gag 1169
 Gly Ala Asp Ala Gly Ala Val Thr Gln Glu Glu Glu Asn Pro Val Glu
 345 350 355 360
 cta tgg agc tta gat gag atc aat ttc atg ctg gaa gga gac ttt 1214
 Leu Trp Ser Leu Asp Glu Ile Asn Phe Met Leu Glu Gly Asp Phe
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 tgaagtgc gatggttct tagtttgtaa ataaagctgt gttggatttt gctgttgggg 1274
 gatggtacaa gtcacacctc aagctctatg cattggtatc tcatgagcct tctctccat 1334
 agagagtctc tcttttaatt ttgtcgaaat aaaaaagggt tgatgaagta aatagaggta 1394
 taataatatac tatctattaa gtcttggttt gtcttttcat ttttgtattt cttttctatt 1454
 taaaagacag tttattatgc ttctgagctc tctttttgat ctttgttata gcgtatcatc 1514
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Lys	Ala	Ser	Lys	Lys	Arg	Ser	Asn	Lys	Arg	Ser	Asp	Phe	Phe	Asp	Leu	
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Phe	Asp	Cys	Glu	Asp	Asp	Asp	Asp	Val	Phe	Val	Asn	Val	Lys	Pro	Phe	
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Val	Gly	Ser	Ala	Tyr	Ala	Lys	Lys	Thr	Val	Glu	Ser	Ala	Glu	Gln	Ala	
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Glu	Lys	Ser	Ser	Lys	Arg	Lys	Arg	Lys	Asn	Gln	Tyr	Arg	Gly	Ile	Arg	
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Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Arg	Lys	
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Gly	Ser	Arg	Glu	Trp	Leu	Gly	Thr	Phe	Asp	Thr	Ala	Glu	Glu	Ala	Ala	
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Arg	Ala	Tyr	Asp	Ala	Ala	Ala	Arg	Arg	Ile	Arg	Gly	Thr	Lys	Ala	Lys	
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Val	Asn	Phe	Pro	Glu	Glu	Lys	Asn	Pro	Ser	Val	Val	Ser	Gln	Lys	Arg	
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Pro	Ser	Ala	Lys	Thr	Asn	Asn	Leu	Gln	Lys	Ser	Val	Ala	Lys	Pro	Asn	
		195			200						205					
Lys	Ser	Val	Thr	Leu	Val	Gln	Gln	Pro	Thr	His	Leu	Ser	Gln	Gln	Tyr	
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Cys	Asn	Asn	Ser	Phe	Asp	Asn	Ser	Phe	Gly	Asp	Met	Ser	Phe	Met	Glu	
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Glu	Lys	Pro	Gln	Met	Tyr	Asn	Asn	Gln	Phe	Gly	Leu	Thr	Asn	Ser	Phe	
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Ser	Asn	Ser	Phe	Asp	Cys	Ser	Glu	Phe	Gly	Trp	Ser	Asp	His	Gly	Pro	
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Lys	Thr	Pro	Glu	Ile	Ser	Ser	Met	Leu	Val	Asn	Asn	Asn	Glu	Ala	Ser	
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Phe	Val	Glu	Glu	Thr	Asn	Ala	Ala	Lys	Lys	Leu	Lys	Pro	Asn	Ser	Asp	
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Thr	Phe	Leu	Thr	Gln	Pro	Phe	Ser	Tyr	Gly	Ser	Asp	Leu	Gln	Gln	Thr	
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ggg	tca	tta	atc	gga	ctc	aac	aac	ctc	tct	tct	tct	cag	atc	cac	cag	707
Gly	Ser	Leu	Ile	Gly	Leu	Asn	Asn	Leu	Ser	Ser	Ser	Gln	Ile	His	Gln	
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atc	cag	tct	cag	atc	cat	cat	cct	ctt	cct	cgc	acg	cat	cac	aac	aac	755
Ile	Gln	Ser	Gln	Ile	His	His	Pro	Leu	Pro	Pro	Thr	His	His	Asn	Asn	
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aac	aac	tct	ttc	tcg	aat	ctt	ctc	agc	cca	aag	cgc	tta	ctg	atg	aag	803
Asn	Asn	Ser	Phe	Ser	Asn	Leu	Leu	Ser	Pro	Lys	Pro	Leu	Leu	Met	Lys	
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caa	tct	gga	gtc	gct	gga	tct	tgt	ttc	gct	tac	ggg	tca	ggg	gtt	cct	851
Gln	Ser	Gly	Val	Ala	Gly	Ser	Cys	Phe	Ala	Tyr	Gly	Ser	Gly	Val	Pro	
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tcg	aag	cgc	acg	aag	ctt	tac	aga	ggg	gtg	agg	caa	cgt	cac	tgg	gga	899
Ser	Lys	Pro	Thr	Lys	Leu	Tyr	Arg	Gly	Val	Arg	Gln	Arg	His	Trp	Gly	
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Lys	Trp	Val	Ala	Glu	Ile	Arg	Leu	Pro	Arg	Asn	Arg	Thr	Arg	Leu	Trp	
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ctt	ggg	act	ttt	gac	acg	gcg	gag	gaa	gct	gcg	ttg	gcc	tat	gat	aag	995
Leu	Gly	Thr	Phe	Asp	Thr	Ala	Glu	Glu	Ala	Ala	Leu	Ala	Tyr	Asp	Lys	
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gcg	gcg	tac	aag	ctg	cgc	ggc	gat	ttc	gcc	cgg	ctt	aac	ttc	cct	aac	1043
Ala	Ala	Tyr	Lys	Leu	Arg	Gly	Asp	Phe	Ala	Arg	Leu	Asn	Phe	Pro	Asn	
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cta	cgt	cat	aac	gga	ttt	cac	atc	gga	ggc	gat	ttc	ggg	gaa	tat	aaa	1091
Leu	Arg	His	Asn	Gly	Phe	His	Ile	Gly	Gly	Asp	Phe	Gly	Glu	Tyr	Lys	
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cct	ctt	cac	tcg	tca	gtc	gac	gct	aag	ctt	gaa	gct	att	tgt	aaa	agc	1139
Pro	Leu	His	Ser	Ser	Val	Asp	Ala	Lys	Leu	Glu	Ala	Ile	Cys	Lys	Ser	
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atg	gcg	gag	act	cag	aaa	cag	gac	aaa	tcg	acg	aaa	tca	tcg	aag	aaa	1187
Met	Ala	Glu	Thr	Gln	Lys	Gln	Asp	Lys	Ser	Thr	Lys	Ser	Ser	Lys	Lys	
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cgt	gag	aag	aag	gtt	tcg	tcg	cca	gat	cta	tcg	gag	aaa	gtg	aag	gcg	1235
Arg	Glu	Lys	Lys	Val	Ser	Ser	Pro	Asp	Leu	Ser	Glu	Lys	Val	Lys	Ala	
																260
gag	gag	aat	tcg	gtt	tcg	atc	ggg	gga	tct	cca	cgc	gtg	acg	gag	ttt	1283
Glu	Glu	Asn	Ser	Val	Ser	Ile	Gly	Gly	Ser	Pro	Pro	Val	Thr	Glu	Phe	
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gaa gag tcc acc gct gga tct tcg ccg ttg tcg gac ttg acg ttc gct 1331
 Glu Glu Ser Thr Ala Gly Ser Ser Pro Leu Ser Asp Leu Thr Phe Ala
 290 295 300 305

gac ccg gag gag ccg ccg cag tgg aac gag acg ttc tcg ttg gag aag 1379
 Asp Pro Glu Glu Pro Pro Gln Trp Asn Glu Thr Phe Ser Leu Glu Lys
 310 315 320

tat ccg tcg tac gag atc gat tgg gat tcg att cta gct taggggcaaa 1428
 Tyr Pro Ser Tyr Glu Ile Asp Trp Asp Ser Ile Leu Ala
 325 330

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aattaattaa atatggatta gtgttaaatt tcgtatgtta atatttgtat tatggtttgt 1548

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 35 40 45

His Pro Ser Ala Phe Ser Leu Pro Pro Leu Pro Gly Tyr Tyr Pro Asp
 50 55 60

Ser Thr Phe Leu Thr Gln Pro Phe Ser Tyr Gly Ser Asp Leu Gln Gln
 65 70 75 80

Thr Gly Ser Leu Ile Gly Leu Asn Asn Leu Ser Ser Ser Gln Ile His
 85 90 95

Gln Ile Gln Ser Gln Ile His His Pro Leu Pro Pro Thr His His Asn
 100 105 110

Asn Asn Asn Ser Phe Ser Asn Leu Leu Ser Pro Lys Pro Leu Leu Met
 115 120 125

Lys Gln Ser Gly Val Ala Gly Ser Cys Phe Ala Tyr Gly Ser Gly Val
 130 135 140

Pro Ser Lys Pro Thr Lys Leu Tyr Arg Gly Val Arg Gln Arg His Trp
145 150 155 160

Gly Lys Trp Val Ala Glu Ile Arg Leu Pro Arg Asn Arg Thr Arg Leu
165 170 175

Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp
180 185 190

Lys Ala Ala Tyr Lys Leu Arg Gly Asp Phe Ala Arg Leu Asn Phe Pro
195 200 205

Asn Leu Arg His Asn Gly Phe His Ile Gly Gly Asp Phe Gly Glu Tyr
210 215 220

Lys Pro Leu His Ser Ser Val Asp Ala Lys Leu Glu Ala Ile Cys Lys
225 230 235 240

Ser Met Ala Glu Thr Gln Lys Gln Asp Lys Ser Thr Lys Ser Ser Lys
245 250 255

Lys Arg Glu Lys Lys Val Ser Ser Pro Asp Leu Ser Glu Lys Val Lys
260 265 270

Ala Glu Glu Asn Ser Val Ser Ile Gly Gly Ser Pro Pro Val Thr Glu
275 280 285

Phe Glu Glu Ser Thr Ala Gly Ser Ser Pro Leu Ser Asp Leu Thr Phe
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305 310 315 320

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325 330

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<223> G8

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cgatcatctc gagctcttcg tgagagatta tgtgattatg taatcggttg tgctgtagaa 180

gacgatctct aacaactgat tccttcatca tcaccttcgc tagatttgta attttcagag 240

cttgag atg ttg gat ctt aac ctc aac gct gat tct ccc gag tgg act	288
Met Leu Asp Leu Asn Leu Asn Ala Asp Ser Pro Glu Ser Thr	
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cag tac ggt ggt gac tca tac tta gat cgg cag aca tca gac aac tcc	336
Gln Tyr Gly Gly Asp Ser Tyr Leu Asp Arg Gln Thr Ser Asp Asn Ser	
15 20 25 30	
gcc ggg aat cga gtg gaa gag tcc ggt aca tgg acg tgg tca gtt atc	384
Ala Gly Asn Arg Val Glu Glu Ser Gly Thr Ser Ser Ser Val Ile	
35 40 45	
aat gcc gat gga gac gaa gac tct tgc tct act cga gct ttc act ctc	432
Asn Ala Asp Gly Asp Glu Asp Ser Cys Ser Thr Arg Ala Phe Thr Leu	
50 55 60	
agt ttc gat att tta aaa gtc gga agt agc ggc gga gac gaa agc	480
Ser Phe Asp Ile Leu Lys Val Gly Ser Ser Ser Gly Gly Asp Glu Ser	
65 70 75	
ccc gcc gct tca gct tcc gtt act aaa gag ttt ttt ccg gtg agt gga	528
Pro Ala Ala Ser Ala Ser Val Thr Lys Glu Phe Phe Pro Val Ser Gly	
80 85 90	
gac tgt gga cat cta cga gat gtt gaa gga tca tca agc tct aga aac	576
Asp Cys Gly His Leu Arg Asp Val Glu Gly Ser Ser Ser Arg Asn	
95 100 105 110	
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Trp Ile Asp Leu Ser Phe Asp Arg Ile Gly Asp Gly Glu Thr Lys Leu	
115 120 125	
gta act ccg gtt ccg act ccg gct ccg gtt ccg gct cag gtt aaa aag	672
Val Thr Pro Val Pro Thr Pro Ala Pro Val Pro Ala Gln Lys Lys	
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Ser Arg Arg Gly Pro Arg Ser Arg Ser Ser Gln Tyr Arg Gly Val Thr	
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Phe Tyr Arg Arg Thr Gly Arg Trp Glu Ser His Ile Trp Asp Cys Gly	
160 165 170	
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Lys Gln Val Tyr Leu Gly Gly Phe Asp Thr Ala His Ala Ala Arg	
175 180 185 190	
gct tat gat cga gct gct att aaa ttt aga ggt gtt gat gct gat atc	864
Ala Tyr Asp Arg Ala Ala Ile Lys Phe Arg Gly Val Asp Ala Asp Ile	
195 200 205	
aac ttt act ctt ggt gat tat gag gaa gat atg aaa cag gta caa aac	912
Asn Phe Thr Leu Gly Asp Tyr Glu Glu Asp Met Lys Gln Val Gln Asn	
210 215 220	

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ggt Gly 255	aga Arg	tgg Trp	gaa Glu	gct Ala	agg Arg 260	atg Met	ggg Gly	cag Gln	ttt Phe	ctt Leu 265	ggt Gly	aaa Lys	aag Lys	gct Ala	tat Tyr 270	1056
gac Asp	aag Lys	gct Ala	gca Ala	atc Ile 275	aac Asn	act Thr	aat Asn	ggt Gly	aga Arg 280	gaa Glu	gca Ala	gtc Val	acg Thr	aac Asn 285	ttc Phe	1104
gag Glu	atg Met	agt Ser	tca Tyr 290	tac Tyr	caa Gln	aat Asn	gag Glu	att Ile 295	aac Asn	tct Ser	gag Glu	agc Ser	aat Asn 300	aac Asn	tct Ser	1152
gag Glu	att Ile 305	gac Asp	ctc Leu	aac Asn	ttg Leu	gga Gly	atc Ile 310	tct Ile	tta Leu	tcg Ser	acc Thr	ggt Gly 315	aat Asn	gcg Ala	cca Pro	1200
aag Lys	caa Gln 320	aat Asn	ggg Gly	agg Arg	ctc Leu	ttt Phe 325	cac His	ttc Phe	cct Pro	tct Ser	aat Ser 330	act Thr	tat Tyr	gaa Glu	act Thr	1248
cag Gln 335	cgt Arg	gga Gly	gtt Val	agc Ser	ttg Leu 340	agg Arg	ata Ile	gat Asp	aac Asn	gaa Glu 345	tac Tyr	atg Met	gga Gly	aag Lys	ccg Pro 350	1296
gtg Val	aat Asn	aca Thr	cct Pro 355	ctt Leu	cct Pro	tat Tyr	gga Gly	tcg Ser	gat Ser 360	cat His	cgc Arg	ctt Leu	tac Tyr 365	tgg Trp		1344
aac Asn	gga Gly	gca Ala	tcg Cys 370	ccg Pro	agt Ser	tat Tyr	aat Asn 375	aat Asn	ccc Pro	gcc Ala	gag Glu	gga Gly	aga Ala 380	gca Ala	aca Thr	1392
gaa Glu	aag Lys 385	aga Arg	agt Ser	gaa Glu	gct Ala	gaa Glu 390	ggg Gly	atg Met	atg Met	agt Ser	aac Asn	tgg Trp 395	gga Gly	tgg Trp	cag Gln	1440
aga Arg 400	ccg Pro	ggg Gly	caa Gln	aca Thr	agc Ser	gcc Ala 405	gtg Val	aga Ala	ccg Pro	cag Gln	cca Pro 410	ccg Pro	gga Gly	cca Pro	caa Gln	1488
cca Pro 415	cca Pro	cca Pro	ttg Leu	ttc Phe	tca Ser 420	gtt Val	gca Ala	gca Ala	gca Ala	tca Ser 425	tca Ser	gga Gly	ttc Phe	tca Ser	cat His 430	1536
ttc Phe	cgg Pro	cca Pro	caa Pro	cct Pro 435	ccc Pro	aat Asn	gac Asp	aat Asn	gca Ala 440	aca Thr	cgt Arg	ggt Gly	tac Tyr	ttt Phe 445	tat Tyr	1584
cca Pro 445	cac His	cct Pro	taact	gtg	taa	gggg	acatat	gag	agttttt	ttacc	atctc					1633

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<220>
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 35 40 45
 Asp Gly Asp Glu Asp Ser Cys Ser Thr Arg Ala Phe Thr Leu Ser Phe
 50 55 60
 Asp Ile Leu Lys Val Gly Ser Ser Ser Gly Gly Asp Glu Ser Pro Ala
 65 70 75 80
 Ala Ser Ala Ser Val Thr Lys Glu Phe Phe Pro Val Ser Gly Asp Cys
 85 90 95
 Gly His Leu Arg Asp Val Glu Gly Ser Ser Ser Arg Asn Trp Ile
 100 105 110
 Asp Leu Ser Phe Asp Arg Ile Gly Asp Gly Glu Thr Lys Leu Val Thr
 115 120 125
 Pro Val Pro Thr Pro Ala Pro Val Pro Ala Gln Val Lys Lys Ser Arg
 130 135 140
 Arg Gly Pro Arg Ser Arg Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr
 145 150 155 160
 Arg Arg Thr Gly Arg Trp Glu Ser His Ile Trp Asp Cys Gly Lys Gln
 165 170 175
 Val Tyr Leu Gly Gly Phe Asp Thr Ala His Ala Ala Ala Arg Ala Tyr
 180 185 190
 Asp Arg Ala Ala Ile Lys Phe Arg Gly Val Asp Ala Asp Ile Asn Phe
 195 200 205
 Thr Leu Gly Asp Tyr Glu Glu Asp Met Lys Gln Val Gln Asn Leu Ser
 210 215 220

Lys Glu Glu Phe Val His Ile Leu Arg Arg Gln Ser Thr Gly Phe Ser
 225 230 235 240
 Arg Gly Ser Ser Lys Tyr Arg Gly Val Thr Leu His Lys Cys Gly Arg
 245 250 255
 Trp Glu Ala Arg Met Gly Gln Phe Leu Gly Lys Lys Ala Tyr Asp Lys
 260 265 270
 Ala Ala Ile Asn Thr Asn Gly Arg Glu Ala Val Thr Asn Phe Glu Met
 275 280 285
 Ser Ser Tyr Gln Asn Glu Ile Asn Ser Glu Ser Asn Asn Ser Glu Ile
 290 295 300
 Asp Leu Asn Leu Gly Ile Ser Leu Ser Thr Gly Asn Ala Pro Lys Gln
 305 310 315 320
 Asn Gly Arg Leu Phe His Phe Pro Ser Asn Thr Tyr Glu Thr Gln Arg
 325 330 335
 Gly Val Ser Leu Arg Ile Asp Asn Glu Tyr Met Gly Lys Pro Val Asn
 340 345 350
 Thr Pro Leu Pro Tyr Gly Ser Ser Asp His Arg Leu Tyr Trp Asn Gly
 355 360 365
 Ala Cys Pro Ser Tyr Asn Asn Pro Ala Glu Gly Arg Ala Thr Glu Lys
 370 375 380
 Arg Ser Glu Ala Glu Gly Met Met Ser Asn Trp Gly Trp Gln Arg Pro
 385 390 395 400
 Gly Gln Thr Ser Ala Val Arg Pro Gln Pro Gly Pro Gln Pro Pro
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Ser	Thr	Ser	Glu	Ser	Phe	Ser	Ala	Thr	Thr	Ala	Lys	Lys	Leu	Ser	Pro	
		15						20					25			
cct	ccc	gcg	gcg	gcy	tta	cgc	ctc	tac	cgg	atg	gga	agc	ggc	ggg	agc	209
Pro	Pro	Ala	Ala	Ala	Leu	Arg	Leu	Tyr	Arg	Met	Gly	Ser	Gly	Gly	Ser	
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agc	gtc	gtg	ttg	gat	ccc	gag	aac	ggc	cta	gag	acg	gag	tca	cga	aag	257
Ser	Val	Val	Leu	Asp	Pro	Glu	Asn	Gly	Leu	Glu	Thr	Glu	Ser	Arg	Lys	
	45					50					55					
cta	cca	tct	tca	aaa	tac	aaa	ggt	gtt	gtt	cct	cag	cct	aac	gga	aga	305
Leu	Pro	Ser	Ser	Lys	Tyr	Lys	Gly	Val	Val	Pro	Gln	Pro	Asn	Gly	Arg	
	60				65					70				75		
tgg	gga	gct	cag	atc	tac	gag	aag	cac	caa	cga	gta	tgg	ctc	ggg	act	353
Trp	Gly	Ala	Gln	Ile	Tyr	Glu	Lys	His	Gln	Arg	Val	Trp	Leu	Gly	Thr	
			80						85				90			
ttc	aac	gag	caa	gaa	gaa	gct	gct	cgt	tcc	tac	gac	atc	gca	gct	tgt	401
Phe	Asn	Glu	Gln	Glu	Glu	Ala	Ala	Arg	Ser	Tyr	Asp	Ile	Ala	Ala	Cys	
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Arg	Phe	Arg	Gly	Arg	Asp	Ala	Val	Val	Asn	Phe	Lys	Asn	Val	Leu	Glu	
		110				115						120				
gac	ggc	gat	tta	gct	ttt	ctt	gaa	gct	cac	tca	aag	gcc	gag	atc	gtc	497
Asp	Gly	Asp	Leu	Ala	Phe	Leu	Glu	Ala	His	Ser	Lys	Ala	Glu	Ile	Val	
	125					130					135					
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Asp	Met	Leu	Arg	Lys	His	Thr	Tyr	Ala	Asp	Glu	Leu	Glu	Gln	Asn	Asn	
	140			145						150				155		
aaa	cgg	cag	ttg	ttt	ctc	tcc	gtc	gac	gct	aac	gga	aaa	cgt	aac	gga	593
Lys	Arg	Gln	Leu	Phe	Leu	Ser	Val	Asp	Ala	Asn	Gly	Lys	Arg	Asn	Gly	
			160					165					170			
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Ser	Ser	Thr	Thr	Gln	Asn	Asp	Lys	Val	Leu	Lys	Thr	Cys	Glu	Val	Leu	
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Phe	Glu	Lys	Ala	Val	Thr	Pro	Ser	Asp	Val	Gly	Lys	Leu	Asn	Arg	Leu	
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tca ccg gca gtg act aaa gga gtt ttg atc aac ttc gaa gac gtt aac 785
 Ser Pro Ala Val Thr Lys Gly Val Leu Ile Asn Phe Glu Asp Val Asn 235
 220 225 230

ggt aaa gtg tgg agg ttc cgt tac tca tac tgg aac agt agt caa agt 833
 Gly Lys Val Trp Arg Phe Arg Tyr Ser Arg Trp Asn Ser Ser Gln Ser 250
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tac gtg ttg acc aag gga tgg agt cga ttc gtc aag gag aag aat ctt 881
 Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Asn Leu 265
 255 260

cga gcc ggt gat gtt gtt act ttc gag aga tgc acc gga cta gag cgg 929
 Arg Ala Gly Asp Val Val Thr Phe Glu Arg Ser Thr Gly Leu Glu Arg 280
 270 275

cag tta tat att gat tgg aaa gtt cgg tct ggt ccg aga gaa aac ccg 977
 Gln Leu Tyr Ile Asp Trp Lys Val Arg Ser Gly Pro Arg Glu Asn Pro 295
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gtt cag gtg gtg gtt cgg ctt ttc gga gtt gat atc ttt aat gtg acc 1025
 Val Gln Val Val Val Arg Leu Phe Gly Val Asp Ile Phe Asn Val Thr 315
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acc gtg aag cca aac gac gtc gtg gcc gtt tgc ggt gga aag aga tct 1073
 Thr Val Lys Pro Asn Asp Val Val Ala Val Cys Gly Gly Lys Arg Ser 330
 320 325

cga gat gtt gat gat atg ttt gcg tta cgg tgt tcc aag aag cag gcg 1121
 Arg Asp Val Asp Asp Met Phe Ala Leu Arg Cys Ser Lys Lys Gln Ala 345
 335 340

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Tyr	Glu	Lys	His	Gln	Arg	Val	Trp	Leu	Gly	Thr	Phe	Asn	Glu	Gln	Glu
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Glu	Ala	Ala	Arg	Ser	Tyr	Asp	Ile	Ala	Ala	Cys	Arg	Phe	Arg	Gly	Arg
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Asp	Ala	Val	Val	Asn	Phe	Lys	Asn	Val	Leu	Glu	Asp	Gly	Asp	Leu	Ala
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Phe	Arg	Tyr	Ser	Tyr	Trp	Asn	Ser	Ser	Gln	Ser	Tyr	Val	Leu	Thr	Lys
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Gly	Trp	Ser	Arg	Phe	Val	Lys	Glu	Lys	Asn	Leu	Arg	Ala	Gly	Asp	Val
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							280					285			
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						295					300				
Arg	Leu	Phe	Gly	Val	Asp	Ile	Phe	Asn	Val	Thr	Thr	Val	Lys	Pro	Asn
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Asp	Val	Val	Ala	Val	Cys	Gly	Gly	Lys	Arg	Ser	Arg	Asp	Val	Asp	Asp
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Met Thr Glu Lys Pro Lys Arg Asn Leu Ile Ser Ser Asn Glu Lys Arg
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Tyr Lys Gly Ile Arg Met Arg Lys Trp Gly Lys Trp Val Ala Glu Ile
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aga gag cct aat aaa cga tca cgg atc tgg ctt ggt tca tac aaa acc 199
Arg Glu Pro Asn Lys Arg Ser Arg Ile Trp Leu Gly Ser Tyr Lys Thr
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gcc gtt gcc gcg gca cgg gcc tac gat acc gct gtg ttt tac tta cgt 247
Ala Val Ala Ala Ala Arg Ala Tyr Asp Thr Ala Val Phe Tyr Leu Arg
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Gly Pro Ser Ala Arg Leu Asn Phe Pro Glu Glu Val Phe Lys Asp Gly
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aac ggc ggt gaa ggc tta gga gga gat atg tct ccg acg ttg ata cgg 343
Asn Gly Gly Glu Gly Leu Gly Gly Asp Met Ser Pro Thr Leu Ile Arg
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aag aag gcg gct gag gtg gga gct aga gtc gac gca gag ttg cgg tta 391
Lys Lys Ala Ala Glu Val Gly Ala Arg Val Asp Ala Glu Leu Arg Leu
               105               110               115

gag aat agg atg gtt gag aac tta gac atg aat aag ttg ccg gag gca 439
Glu Asn Arg Met Val Glu Asn Leu Asp Met Asn Lys Leu Pro Glu Ala
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Tyr Gly Leu

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atttttgttt tgagcatagat aattatgtca taacc 583

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 35 40 45
 Trp Leu Gly Ser Tyr Lys Thr Ala Val Ala Ala Arg Ala Tyr Asp
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 Thr Ala Val Phe Tyr Leu Arg Gly Pro Ser Ala Arg Leu Asn Phe Pro
 65 70 75 80
 Glu Glu Val Phe Lys Asp Gly Asn Gly Gly Glu Gly Leu Gly Gly Asp
 85 90 95
 Met Ser Pro Thr Leu Ile Arg Lys Lys Ala Ala Glu Val Gly Ala Arg
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 Met Cys Gly Gly Ala Ile
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 ata tcc gat ttc att cca ccg ccg agg tct cgc cgt gtt act agc gag 164
 Ile Ser Asp Phe Ile Pro Pro Pro Arg Ser Arg Arg Val Thr Ser Glu
 10 15 20

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 Phe Ile Trp Pro Asp Leu Lys Lys Asn Leu Lys Gly Ser Lys Lys Ser
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 tcg aag aat cgt tcg aat ttc ttc gat ttt gac gct gag ttc gaa gct 260
 Ser Lys Asn Arg Ser Asn Phe Phe Asp Phe Asp Ala Glu Phe Glu Ala
 40 45 50
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 Asp Phe Gln Gly Phe Lys Asp Asp Ser Ser Ile Asp Cys Asp Asp Asp
 55 60 65 70
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 Phe Asp Val Gly Asp Val Phe Ala Asp Val Lys Pro Phe Val Phe Thr
 75 80 85
 tcg act cca aaa ccc gcc gtc tcc gcc gct gcg gaa ggt tca gtt ttt 404
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 Gly Lys Lys Val Thr Gly Leu Asp Gly Asp Ala Glu Lys Ser Ala Asn
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 120 125 130
 aaa tgg gct gct gag ata cgt gat cca agg gaa ggt gct aga atc tgg 548
 Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Glu Gly Ala Arg Ile Trp
 135 140 145 150
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 155 160 165
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 170 175 180
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 185 190 195
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 Gln Lys Pro Val Ala Lys Pro Asn Pro Asn Pro Ser Pro Ala Leu Val
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 cag aac tcg aac atc tcc ttt gaa aat atg tgt ttc atg gag gag aaa 788
 Gln Asn Ser Asn Ile Ser Phe Glu Asn Met Cys Phe Met Glu Glu Lys
 215 220 225 230
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 His Gln Val Ser Asn Asn Asn Asn Asn Gln Phe Gly Met Thr Asn Ser
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agt aat tct ttc gat tgt tgg gag ttt ggt tgg agc gat caa gct ccg 932
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 265 270 275

ata act ccc gac atc tct tct gcg gtt atc aac aac aac aac tca gct 980
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 280 285 290

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 295 300 305 310

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 315 320 325

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 35 40 45

Asp Ala Glu Phe Glu Ala Asp Phe Gln Gly Phe Lys Asp Asp Ser Ser
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 Ile Asp Cys Asp Asp Phe Asp Val Gly Asp Val Phe Ala Asp Val
 65 70 75 80
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 85 90 95
 Ala Glu Gly Ser Val Phe Gly Lys Lys Val Thr Gly Leu Asp Gly Asp
 100 105 110
 Ala Glu Lys Ser Ala Asn Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile
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 145 150 155 160
 Ala Arg Ala Tyr Asp Ala Ala Ala Arg Arg Ile Arg Gly Ser Lys Ala
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 Lys Val Asn Phe Pro Glu Glu Asn Met Lys Ala Asn Ser Gln Lys Arg
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 Ser Val Lys Ala Asn Leu Gln Lys Pro Val Ala Lys Pro Asn Pro Asn
 195 200 205
 Pro Ser Pro Ala Leu Val Gln Asn Ser Asn Ile Ser Phe Glu Asn Met
 210 215 220
 Cys Phe Met Glu Glu Lys His Gln Val Ser Asn Asn Asn Asn Asn Gln
 225 230 235 240
 Phe Gly Met Thr Asn Ser Val Asp Ala Gly Cys Asn Gly Tyr Gln Tyr
 245 250 255
 Phe Ser Ser Asp Gln Gly Ser Asn Ser Phe Asp Cys Ser Glu Phe Gly
 260 265 270
 Trp Ser Asp Gln Ala Pro Ile Thr Pro Asp Ile Ser Ser Ala Val Ile
 275 280 285
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 Lys Leu Lys Ser Met Asp Phe Glu Thr Pro Tyr Asn Asn Thr Glu Trp
 305 310 315 320
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Arg Ile Lys Phe Thr Glu His Lys Thr Asn Thr Thr Thr Ile Val Ser
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gag tta acc aac act cac caa acc agg att ctt cgt atc tca gtc act 628
Glu Leu Thr Asn Thr His Gln Thr Arg Ile Leu Arg Ile Ser Val Thr
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Asp Pro Asp Ala Thr Asp Ser Ser Ser Asp Asp Glu Glu Glu Glu His
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Gln Arg Phe Val Ser Lys Arg Arg Arg Val Lys Lys Phe Val Asn Glu
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gtc tat ctc gat tcc ggt gct gtt gtt act ggt agt tgt ggt caa atg 772
Val Tyr Leu Asp Ser Gly Ala Val Val Thr Gly Ser Cys Gly Gln Met
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Glu Ser Lys Lys Arg Gln Lys Arg Ala Val Lys Ser Glu Ser Thr Val
95 100 105

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Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg	
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Glu Glu Ala Ala Met Val Tyr Asp Asn Ala Ala Ile Gln Leu Arg Gly	
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 50 55 60
 Arg Arg Arg Val Lys Lys Phe Val Asn Glu Val Tyr Leu Asp Ser Gly
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 Ala Val Val Thr Gly Ser Cys Gly Gln Met Glu Ser Lys Lys Arg Gln
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 Lys Arg Ala Val Lys Ser Glu Ser Thr Val Ser Pro Val Val Ser Ala
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 Thr Thr Thr Thr Thr Gly Glu Lys Lys Phe Arg Gly Val Arg Gln Arg
 115 120 125
 Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Leu Lys Arg Val
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 Tyr Asp Asn Ala Ala Ile Gln Leu Arg Gly Pro Asp Ala Leu Thr Asn
 165 170 175
 Phe Ser Val Thr Pro Thr Thr Ala Thr Glu Lys Lys Ala Pro Pro Pro
 180 185 190

Ser Pro Val Lys Lys Lys Lys Lys Lys Asn Asn Lys Ser Lys Lys Ser
195 200 205

Val Thr Ala Ser Ser Ser Ile Ser Arg Ser Ser Ser Asn Asp Cys Leu
210 215 220

Cys Ser Pro Val Ser Val Leu Arg Ser Pro Phe Ala Val Asp Glu Phe
225 230 235 240

Ser Gly Ile Ser Ser Ser Pro Val Ala Ala Val Val Val Lys Glu Leu
245 250 255

Pro Ser Met Thr Thr Val Ser Glu Thr Phe Ser Asp Phe Ser Ala Pro
260 265 270

Leu Phe Ser Asp Asp Asp Val Phe Asp Phe Arg Ser Ser Val Val Pro
275 280 285

Asp Tyr Leu Gly Gly Asp Leu Phe Gly Glu Asp Leu Phe Thr Ala Asp
290 295 300

Met Cys Thr Asp Met Asn Phe Gly Phe Asp Phe Gly Ser Gly Leu Ser
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cacacctatt attctcttgg tgtgtttgtg tgttacatat acgtgtgagt acatactttg 180

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agc cgt gtc ata gag aat ccg aca gac ccg ccg gtc aaa caa gag ctt 344

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His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu	
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Ile Arg Asp Pro Lys Lys Ala Ala Arg Val Trp Leu Gly Thr Phe Glu	
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Arg Arg Gly Pro Arg Ser Arg Ser Gln Tyr Arg Gly Val Thr Phe
  115         120         125

Tyr Arg Arg Thr Gly Arg Trp Glu Ser His Ile Trp Asp Cys Gly Lys
  130         135         140

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Gln Val Tyr Leu Gly Gly Phe Asp Thr Ala Tyr Ala Ala Ala Arg Ala
 145 150 155 160
 Tyr Asp Arg Ala Ala Ile Lys Phe Arg Gly Leu Asp Ala Asp Ile Asn
 165 170 175
 Phe Val Val Asp Tyr Arg His Asp Ile Asp Lys Met Lys Asn Leu
 180 185 190
 Asn Lys Val Glu Phe Val Gln Thr Leu Arg Arg Glu Ser Ala Ser Phe
 195 200 205
 Gly Arg Gly Ser Ser Lys Tyr Lys Gly Leu Ala Leu Gln Lys Cys Thr
 210 215 220
 Gln Phe Lys Thr His Asp Gln Ile His Leu Phe Gln Asn Arg Gly Trp
 225 230 235 240
 Asp Ala Ala Ala Ile Lys Tyr Asn Glu Leu Gly Lys Gly Glu Gly Ala
 245 250 255
 Met Lys Phe Gly Ala His Ile Lys Gly Asn Gly His Asn Asp Leu Glu
 260 265 270
 Leu Ser Leu Gly Ile Ser Ser Ser Ser Glu Ser Ile Lys Leu Thr Thr
 275 280 285
 Gly Asp Tyr Tyr Lys Gly Ile Asn Arg Ser Thr Met Gly Leu Tyr Gly
 290 295 300
 Lys Gln Ser Ser Ile Phe Leu Pro Met Ala Thr Met Lys Pro Leu Lys
 305 310 315 320
 Thr Val Ala Ala Ser Ser Gly Phe Pro Phe Ile Ser Met Thr Ser Ser
 325 330 335
 Ser Ser Ser Met Ser Asn Cys Phe Asp Pro
 340 345

<210> 25
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 <212> DNA
 <213> *Arabidopsis thaliana*

<220>
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 <222> (377)..(1159)
 <223> G974

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 ccccttaga tctgtttatt tccgcctact ttgattcatt tctgttagta atctgtcttt 120
 cgtatagaag aaaactgatt tcttggtttg tattttctta aagagatcaa tcttttttta 180


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tttttgatct tcttgtgttt ttttttcttt gtagaattaa tcgttttgta gggatatttt 240
ttaattccct cctctcagaa atctacacag aggtttttta ttttataaac ctctttttcg 300
attttcttga aaacaaaaaa tctgttcttt tacttttttt acaagaacaa gggaaaaaaa 360
tttcttttta tttagaa atg aca act tct atg gat ttt tac agt aac aaa acg 412
Met Thr Thr Ser Met Asp Phe Tyr Ser Asn Lys Thr
1 5 10
ttt caa caa tct gat cca ttc ggt ggt gaa tta atg gaa gcg ctt tta 460
Phe Gln Gln Ser Asp Pro Phe Gly Gly Glu Leu Met Glu Ala Leu Leu
15 20 25
cct ttt atc aaa agc cct tcc aac gat tca tcc gcg ttt gcg ttc tct 508
Pro Phe Ile Lys Ser Pro Ser Asn Asp Ser Ser Ala Phe Ala Phe Ser
30 35 40
cta ccc gct cca att tca tac ggg tcg gat ctc cac tca ttt tct cac 556
Leu Pro Ala Pro Ile Ser Tyr Gly Ser Asp Leu His Ser Phe Ser His
45 50 55 60
cat ctt agt cct aaa ccg gtc tca atg aaa caa acc ggt act tcc gcg 604
His Leu Ser Pro Lys Pro Val Ser Met Lys Gln Thr Gly Thr Ser Ala
65 70 75
gct aaa ccg acg aag cta tac aga gga gtg aga caa cgt cac tgg gga 652
Ala Lys Pro Thr Lys Leu Tyr Arg Gly Val Arg Gln Arg His Trp Gly
80 85 90
aaa tgg gtg gct gag att cgt tta ccg agg aat cga act cga ctt tgg 700
Lys Trp Val Ala Glu Ile Arg Leu Pro Arg Asn Arg Thr Arg Leu Trp
95 100 105
ctc gga aca ttc gac acg gcg gag gaa gct gct tta gct tat gac aag 748
Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Lys
110 115 120
gcg gcg tat aag ctc cga gga gat ttt gcg cgg ctt aat ttc cct gat 796
Ala Ala Tyr Lys Leu Arg Gly Asp Phe Ala Arg Leu Asn Phe Pro Asp
125 130 135 140
ctc cgt cat aac gac gag tat caa cct ctt caa tca tca gtc gac gct 844
Leu Arg His Asn Asp Glu Tyr Gln Pro Leu Gln Ser Ser Val Asp Ala
145 150 155
aag ctt gaa gct att tgt caa aac tta gct gag acg acg cag aaa cag 892
Lys Leu Glu Ala Ile Cys Gln Asn Leu Ala Glu Thr Thr Gln Lys Gln
160 165 170
gtg aga tca acg aag aag tct tct tct cgg aaa cgt tca tca acc gtc 940
Val Arg Ser Thr Lys Lys Ser Ser Ser Arg Lys Arg Ser Ser Thr Val
175 180 185
gca gtg aaa cta ccg gag gag gac tac tct agc gcc gga tct tcg ccg 988
Ala Val Lys Leu Pro Glu Glu Asp Tyr Ser Ser Ala Gly Ser Ser Pro
190 195 200

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ctg tta acg gag agt tat gga tct ggt gga tct tct tcg ccg ttg tcg 1036
 Leu Leu Thr Glu Ser Tyr Gly Ser Gly Gly Ser Ser Ser Pro Leu Ser
 205 210 215 220

gag ctg acg ttt ggt gat acg gag gag gag att cag ccg ccg tgg aac 1084
 Glu Leu Thr Phe Gly Asp Thr Glu Glu Glu Ile Gln Pro Pro Trp Asn
 225 230 235

gag aac gcg ttg gag aag tat ccg tcg tac gag atc gat tgg gat tcg 1132
 Glu Asn Ala Leu Glu Lys Tyr Pro Ser Tyr Glu Ile Asp Trp Asp Ser
 240 245 250

att ctt cag tgt tcg agt ctt gta aat tagatgttc cataggggta 1179
 Ile Leu Gln Cys Ser Ser Leu Val Asn
 255 260

ttttagggac ttttagagctc tctgcgatgg agtttttgggt cattgcagag attttattat 1239
 tattaagggg gtttgttatg ttaatatcaa ataagtttat ctactttgat gttaattagt 1299
 gttaatctct cgcgcggtcc aagctgtttt tttttggcat gcttcgaccg tgtgagattt 1359
 cttatgtaat tttttagtct ccttgatttt cttagtgtcaa gttaaattgg cacaaaaaaa 1419
 aaaaaaaaa a 1430

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 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G974

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 Asp Pro Phe Gly Gly Glu Leu Met Glu Ala Leu Leu Pro Phe Ile Lys
 20 25 30
 Ser Pro Ser Asn Asp Ser Ser Ala Phe Ala Phe Ser Leu Pro Ala Pro
 35 40 45
 Ile Ser Tyr Gly Ser Asp Leu His Ser Phe Ser His His Leu Ser Pro
 50 55 60
 Lys Pro Val Ser Met Lys Gln Thr Gly Thr Ser Ala Ala Lys Pro Thr
 65 70 75 80
 Lys Leu Tyr Arg Gly Val Arg Gln Arg His Trp Gly Lys Trp Val Ala
 85 90 95
 Glu Ile Arg Leu Pro Arg Asn Arg Thr Arg Leu Trp Leu Gly Thr Phe
 100 105 110

Asp Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Lys Ala Ala Tyr Lys
115 120 125

Leu Arg Gly Asp Phe Ala Arg Leu Asn Phe Pro Asp Leu Arg His Asn
130 135 140

Asp Glu Tyr Gln Pro Leu Gln Ser Ser Val Asp Ala Lys Leu Glu Ala
145 150 155 160

Ile Cys Gln Asn Leu Ala Glu Thr Thr Gln Lys Gln Val Arg Ser Thr
165 170 175

Lys Lys Ser Ser Ser Arg Lys Arg Ser Ser Thr Val Ala Val Lys Leu
180 185 190

Pro Glu Glu Asp Tyr Ser Ser Ala Gly Ser Ser Pro Leu Leu Thr Glu
195 200 205

Ser Tyr Gly Ser Gly Gly Ser Ser Ser Pro Leu Ser Glu Leu Thr Phe
210 215 220

Gly Asp Thr Glu Glu Glu Ile Gln Pro Pro Trp Asn Glu Asn Ala Leu
225 230 235 240

Glu Lys Tyr Pro Ser Tyr Glu Ile Asp Trp Asp Ser Ile Leu Gln Cys
245 250 255

Ser Ser Leu Val Asn
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<210> 27

<211> 795

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (58)..(654)

<223> G975

<220>

<223> "n" at various positions throughout the sequence
may be A, T, C, G, other or unknown

<220>

<223> Xaa at amino acid position 90 is either a Serine
or not present

<400> 27

attactcatc atcaagttcc tactttctct ctgacaaaca tcacagagta agtaaga 57

atg gta cag acg aag aag ttc aga ggt gtc agg caa cgc cat tgg ggt 105
Met Val Gln Thr Lys Lys Phe Arg Gly Val Arg Gln Arg His Trp Gly
1 5 10 15

tct tgg gtc gct gag att cgt cat cct ctc ttg aaa cgg agg att tgg 153
 Ser Trp Val Ala Glu Ile Arg His Pro Leu Leu Lys Arg Arg Ile Trp
 20 25 30

cta ggg acg ttc gag acc gca gag gag gca gca aga gca tac gac gag 201
 Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Glu
 35 40 45

gcc gcc gtt tta atg agc ggc cgc aac gcc aaa acc aac ttt ccc ctc 249
 Ala Ala Val Leu Met Ser Gly Arg Asn Ala Lys Thr Asn Phe Pro Leu
 50 55 60

aac aac aac aac acc gga gaa act tcc gag ggc aaa acc gat att tca 297
 Asn Asn Asn Asn Thr Gly Glu Thr Ser Glu Gly Lys Thr Asp Ile Ser
 65 70 75 80

gct tgg tcc aca atg tca tcc tca aca tma tct tca tgg ctc tct tcc 345
 Ala Ser Ser Thr Met Ser Ser Ser Thr Xaa Ser Ser Ser Leu Ser Ser
 85 90 95

atc ctc agc gcc aaa ctg agg aaa tgc tgc aag tct cct tcc cca tcc 393
 Ile Leu Ser Ala Lys Leu Arg Lys Cys Cys Lys Ser Pro Ser Pro Ser
 100 105 110

ctc acc tgc ctc cgt ctt gac aca gcc agc tcc cat atc ggc gtc tgg 441
 Leu Thr Cys Leu Arg Leu Asp Thr Ala Ser Ser His Ile Gly Val Trp
 115 120 125

cag aaa cgg gcc ggt tca aag tct gac tcc agc tgg gtc atg acg gtg 489
 Gln Lys Arg Ala Gly Ser Lys Ser Asp Ser Ser Trp Val Met Thr Val
 130 135 140

gag cta ggt ccc gca agc tcc tcc caa gag act act agt aaa gct tca 537
 Glu Leu Gly Pro Ala Ser Ser Ser Gln Glu Thr Thr Ser Lys Ala Ser
 145 150 155 160

caa gac gct att ctt gct ccg acc act gaa gtt gaa att ggt ggc agc 585
 Gln Asp Ala Ile Leu Ala Pro Thr Thr Glu Val Glu Ile Gly Gly Ser
 165 170 175

aga gaa gaa gta ttg gat gag gaa gaa aag gtt gct ttg caa atg ata 633
 Arg Glu Glu Val Leu Asp Glu Glu Lys Val Ala Leu Gln Met Ile
 180 185 190

gag gag ctt ctc aat aca aac taaatcttat ttgcttatat atatgtacct 684
 Glu Glu Leu Leu Asn Thr Asn
 195

attttcattg ctgatttaca gccaaaataa tcaattatac cgtgtatttt atagatgttt 744

tatattaaaa gggtgtaga tatananana nnnnnnnnnn ananannnna a 795

<210> 28

<211> 199

<212> PRT

<213> Arabidopsis thaliana

CC-0.15466

≤223> G975

<223> Xaa at amino acid position 90 is either a Serine
or not present

Met Val Gln Thr Lys Lys Phe Arg Gly Val Arg Gln Arg His Trp Gly
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Ser Trp Val Ala Glu Ile Arg His Pro Leu Leu Lys Arg Arg Ile Trp
20 25 30

Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Glu
35 40 45

Ala Ala Val Leu Met Ser Gly Arg Asn Ala Lys Thr Asn Phe Pro Leu
50 55 60

Asn Asn Asn Asn Thr Gly Glu Thr Ser Glu Gly Lys Thr Asp Ile Ser
65 70 75 80

Ala Ser Ser Thr Met Ser Ser Ser Thr Xaa Ser Ser Ser Leu Ser Ser
85 90 95

Ile Leu Ser Ala Lys Leu Arg Lys Cys Cys Lys Ser Pro Ser Pro Ser
100 105 110

Leu Thr Cys Leu Arg Leu Asp Thr Ala Ser Ser His Ile Gly Val Trp
115 120 125

Gln Lys Arg Ala Gly Ser Lys Ser Asp Ser Ser Trp Val Met Thr Val
130 135 140

Glu Leu Gly Pro Ala Ser Ser Ser Gln Glu Thr Thr Ser Lys Ala Ser
145 150 155 160

Gln Asp Ala Ile Leu Ala Pro Thr Thr Glu Val Glu Ile Gly Gly Ser
165 170 175

Arg Glu Glu Val Leu Asp Glu Glu Glu Lys Val Ala Leu Gln Met Ile
180 185 190

Glu Glu Leu Leu Asn Thr Asn
195

<211> 966

<213> Arabidopsis thaliana

<221> CDS

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222 (72)
223 6976

ggt gcg gct gga gcg gcc gtg aag gta ggt caa aag aag gaa gat aaa 638
Gly Ala Ala Gly Ala Ala Val Lys Val Gly Gln Lys Lys Glu Asp Lys
175 180 185

gtt tat gat acg gcg gaa tct tca act atg ggg ttt gtg gat gaa gaa 686
 Val Tyr Asp Thr Ala Glu Ser Ser Thr Met Gly Phe Val Asp Glu Glu
 190 195 200 205

gag cta ttg aac atg cct ggt ttg cta gcg gat atg gcc aaa ggg atg 734
 Glu Leu Leu Asn Met Pro Gly Leu Leu Ala Asp Met Ala Lys Gly Met
 210 215 220

atg gtg gct cca ccg tgg atg gga tct cca ccg tca gat gat tgg cca 782
 Met Val Ala Pro Pro Trp Met Gly Ser Pro Pro Ser Asp Asp Ser Pro
 225 230 235

gag aat tct gat gga gag agc ttg tgg agc tat tgcacgattg aaagcagttt 835
 Glu Asn Ser Asp Gly Glu Ser Leu Trp Ser Tyr
 240 245

aatatctttt ttggatcctt tgttcacggt tatgctagtc atctttgttt ctttatccta 895

tgattgttag agatgatttg ttaaataatat aatcgtaatg attttcacctt ttttttattc 955

aaaaaaaaa a 966

<210> 30

<211> 248

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G976

<220>

<223> Xaa at amino acid position 77 may be various or
 unknown

<400> 30

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 1 5 10 15

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 20 25 30

Asp Ser Leu Ser Asp Ser Ala Thr Cys Glu Asn Pro Cys Pro Leu Asp
 35 40 45

Thr Ile Thr Thr Thr Thr Thr Val Cys Phe Ala Ala Pro Ser Ser
 50 55 60

Thr Ala Ser Gly Asn Asp Ile Asn Thr Leu Met Ala Xaa Asp Thr Asp
 65 70 75 80

Ile Ser Arg Arg Lys Lys Asn Pro Val Tyr Arg Gly Ile Arg Cys Arg
 85 90 95

Ser Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Lys Lys Thr Arg
 100 105 110

Val Trp Leu Gly Thr Tyr Pro Thr Pro Glu Met Ala Ala Ala Tyr
115 120 125

Asp Val Ala Ala Leu Ala Leu Lys Gly Gly Asp Thr Leu Leu Asn Phe
130 135 140

Pro Asp Ser Leu Gly Ser Tyr Pro Ile Pro Ile Ser Ser Ser Ala Ala
145 150 155 160

His Ile Arg Cys Ala Ala Ala Ala Ala Thr Arg Gly Ala Ala
165 170 175

Gly Ala Ala Val Lys Val Gly Gln Lys Lys Glu Asp Lys Val Tyr Asp
180 185 190

Thr Ala Glu Ser Ser Thr Met Gly Phe Val Asp Glu Glu Glu Leu Leu
195 200 205

Asn Met Pro Gly Leu Leu Ala Asp Met Ala Lys Gly Met Met Val Ala
210 215 220

Pro Pro Trp Met Gly Ser Pro Pro Ser Asp Asp Ser Pro Glu Asn Ser
225 230 235 240

Asp Gly Glu Ser Leu Trp Ser Tyr
245

<210> 31

<211> 833

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (46)..(588)

<223> G977

<220>

<223> "n" at various positions throughout the sequence
may be A, T, C, G, other or unknown

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Met Ala Arg Pro
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caa caa cgc ttt cga ggc gtt aga cag agg cat tgg ggc tct tgg gtc 105
Gln Gln Arg Phe Arg Gly Val Arg Gln Arg His Trp Gly Ser Trp Val
5 10 15 20

tcc gaa att cgt cac cct ctc ttg aaa aca aga atc tgg cta ggg acg 153
Ser Glu Ile Arg His Pro Leu Leu Lys Thr Arg Ile Trp Leu Gly Thr
25 30 35

ttt gag aca gcg gag gat gca gca agg gcc tac gac gag gcg gct agg 201
Phe Glu Thr Ala Glu Asp Ala Ala Arg Ala Tyr Asp Glu Ala Ala Arg
40 45 50

cta atg tgt ggc cgc aga gct cgt act aat ttc cca tac aac cct aat 249
 Leu Met Cys Gly Pro Arg Ala Arg Thr Asn Phe Pro Tyr Asn Pro Asn
 55 60 65

gcc att cct act tcc tct tcc aag ctt cta tca gca act ctt acc gct 297
 Ala Ile Pro Thr Ser Ser Ser Lys Leu Leu Ser Ala Thr Leu Thr Ala
 70 75 80

aaa ctc cac aaa tgc tac atg gct tct ctt caa atg acc aag caa acg 345
 Lys Leu His Lys Cys Tyr Met Ala Ser Leu Gln Met Thr Lys Gln Thr
 85 90 95 100

caa aca caa acg caa acg cag acc gca aga tca caa tcc gcg gac agt 393
 Gln Thr Gln Thr Gln Thr Ala Arg Ser Gln Ser Ala Asp Ser
 105 110 115

gac ggt gtg acg gct aac gaa agt cat ttg aac aga gga gta acg gag 441
 Asp Gly Val Thr Ala Asn Glu Ser His Leu Asn Arg Gly Val Thr Glu
 120 125 130

acg aca gag atc aag tgg gaa gat gga aat gcg aat atg caa cag aat 489
 Thr Thr Glu Ile Lys Trp Glu Asp Gly Asn Ala Asn Met Gln Gln Asn
 135 140 145

ttt agg cca ttg gag gaa gat cat atc gag caa atg att gag gag ctg 537
 Phe Arg Pro Leu Glu Glu Asp His Ile Glu Gln Met Ile Glu Glu Leu
 150 155 160

ctt cac tac ggt tcc att gag ctt tgc tct gtt tta cca act cag acg 585
 Leu His Tyr Gly Ser Ile Glu Leu Cys Ser Val Leu Pro Thr Gln Thr
 165 170 175 180

ctg tgagaaatgg ccttgctgt ttagcgtatt cttttcattt ttatttttgt 638
 Leu

ttccacaaaa acggcgctgt aagtgatgag agtagtagtg agagaaggct aatttcaaga 698

cattttgatc tgaattggcc tcttttgaaa cactgattct agtttctata agagcaatcg 758

atcatatgct atgttatgta tagtattata aaaaaatggt attttctgat tnaaaaaaaa 818

aaaaaaaaaa aaaaa 833

<210> 32
 <211> 181
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G977

<400> 32
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Gly Ser Trp Val Ser Glu Ile Arg His Pro Leu Leu Lys Thr Arg Ile
 20 25 30
 Trp Leu Gly Thr Phe Glu Thr Ala Glu Asp Ala Ala Arg Ala Tyr Asp
 35 40 45
 Glu Ala Ala Arg Leu Met Cys Gly Pro Arg Ala Arg Thr Asn Phe Pro
 50 55 60
 Tyr Asn Pro Asn Ala Ile Pro Thr Ser Ser Ser Lys Leu Leu Ser Ala
 65 70 75 80
 Thr Leu Thr Ala Lys Leu His Lys Cys Tyr Met Ala Ser Leu Gln Met
 85 90 95
 Thr Lys Gln Thr Gln Thr Gln Thr Gln Thr Gln Thr Ala Arg Ser Gln
 100 105 110
 Ser Ala Asp Ser Asp Gly Val Thr Ala Asn Glu Ser His Leu Asn Arg
 115 120 125
 Gly Val Thr Glu Thr Thr Glu Ile Lys Trp Glu Asp Gly Asn Ala Asn
 130 135 140
 Met Gln Gln Asn Phe Arg Pro Leu Glu Glu Asp His Ile Glu Gln Met
 145 150 155 160
 Ile Glu Glu Leu Leu His Tyr Gly Ser Ile Glu Leu Cys Ser Val Leu
 165 170 175
 Pro Thr Gln Thr Leu
 180

<210> 33
 <211> 1530
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (60)..(1349)
 <223> G979

<220>
 <223> "n" at various positions throughout the sequence
 may be A, T, C, G, other or unknown

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 atg aag aag cgc tta acc act tcc act tgt tct tct cca tct tcc 107
 Met Lys Lys Arg Leu Thr Thr Ser Thr Cys Ser Ser Ser Pro Ser Ser
 1 5 10 15
 tct gtt tct tct tct act act act tcc tct cct att cag tgg gag gct 155
 Ser Val Ser Ser Ser Thr Thr Thr Ser Ser Pro Ile Gln Ser Glu Ala
 20 25 30

cca agg cct aaa cga gcc aaa agg gct aag aaa tct tct cct tct ggt	203
Pro Arg Pro Lys Arg Ala Lys Arg Ala Lys Lys Ser Ser Pro Ser Gly	
35 40 45	
gat aaa tct cat aac ccg aca agc cct gct tct acc cga cgc agc tct	251
Asp Lys Ser His Asn Pro Thr Ser Pro Ala Ser Thr Arg Arg Ser Ser	
50 55 60	
atc tac aga gga gtc act aga cat aga tgg act ggg aga ttc gag gct	299
Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Phe Glu Ala	
65 70 75 80	
cat ctt tgg gac aaa agc tct tgg aat tcg att cag aac aag aaa ggc	347
His Leu Trp Asp Lys Ser Ser Trp Asn Ser Ile Gln Asn Lys Lys Gly	
85 90 95	
aaa caa gtt tat ctg gga gca tat gac agt gaa gaa gca gca gca cat	395
Lys Gln Val Tyr Leu Gly Ala Tyr Asp Ser Glu Glu Ala Ala Ala His	
100 105 110	
acg tac gat ctg gct gct ctc aag tac tgg gga ccc gac acc atc ttg	443
Thr Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Asp Thr Ile Leu	
115 120 125	
aat ttt ccg gca gag acg tac aca aag gaa ttg gaa gaa atg cag aga	491
Asn Phe Pro Ala Glu Thr Tyr Thr Lys Glu Leu Glu Glu Met Gln Arg	
130 135 140	
gtg aca aag gaa gaa tat ttg gct tct ctc cgc cgc cag agc agt ggt	539
Val Thr Lys Glu Glu Tyr Leu Ala Ser Leu Arg Arg Gln Ser Ser Gly	
145 150 155 160	
ttc tcc aga ggc gtc tct aaa tat cgc ggc gtc gct agg cat cac cac	587
Phe Ser Arg Gly Val Ser Lys Tyr Arg Gly Val Ala Arg His His His	
165 170 175	
aac gga aga tgg gag gct cgg atc gga aga gtg ttt ggg aac aag tac	635
Asn Gly Arg Trp Glu Ala Arg Ile Gly Arg Val Phe Gly Asn Lys Tyr	
180 185 190	
ttg tac ctc ggc acc tat aat acg cag gag gaa gct gct gca gca tat	683
Leu Tyr Leu Gly Thr Tyr Asn Thr Gln Glu Glu Ala Ala Ala Tyr	
195 200 205	
gac atg gct cgc att gag tat cga ggc gca aac cgc gtt act aat ttc	731
Asp Met Ala Ala Ile Glu Tyr Arg Gly Ala Asn Ala Val Thr Asn Phe	
210 215 220	
gac att agt aat tac att gac cgg tta aag aaa ggt gtt ttc cgc	779
Asp Ile Ser Asn Tyr Ile Asp Arg Leu Lys Lys Gly Val Phe Pro	
225 230 235 240	
ttc cct gtg aac caa gct aac cat caa gag ggt att ctt gtt gaa gcc	827
Phe Pro Val Asn Gln Ala Asn His Gln Glu Gly Ile Leu Val Glu Ala	
245 250 255	

aaa caa gaa gtt gaa acg aga gaa gcg aag gaa gag cct aga gaa gaa 875
 Lys Gln Glu Val Glu Thr Arg Glu Ala Lys Glu Glu Pro Arg Glu Glu
 260 265 270
 gtg aaa caa cag tac gtg gaa gaa cca ccg caa gaa gaa gaa gag aag 923
 Val Lys Gln Gln Tyr Val Glu Glu Pro Pro Gln Glu Glu Glu Lys
 275 280 285
 gaa gaa gag aaa gca gag caa caa gaa gca gag att gta gga tat tca 971
 Glu Glu Glu Lys Ala Glu Gln Gln Glu Ala Glu Ile Val Gly Tyr Ser
 290 295 300
 gaa gaa gca gca gtg gtc aat tgc tgc ata gac tct tca acc ata atg 1019
 Glu Glu Ala Ala Val Val Asn Cys Cys Ile Asp Ser Ser Thr Ile Met
 305 310 315 320
 gaa atg gat cgt tgt ggg gac aac aat gag ctg gct tgg aac ttc tgt 1067
 Glu Met Asp Arg Cys Gly Asp Asn Asn Glu Leu Ala Trp Asn Phe Cys
 325 330 335
 atg atg gat aca ggg ttt tct ccg ttt ttg act gat cag aat ctc gcg 1115
 Met Met Asp Thr Gly Phe Ser Pro Phe Leu Thr Asp Gln Asn Leu Ala
 340 345 350
 aat gag aat ccc ata gag tat ccg gag cta ttc aat gag tta gca ttt 1163
 Asn Glu Asn Pro Ile Glu Tyr Pro Glu Leu Phe Asn Glu Leu Ala Phe
 355 360 365
 gag gac aac atc gac ttc atg ttc gat gat ggg aag cac gag tgc ttg 1211
 Glu Asp Asn Ile Asp Phe Met Phe Asp Asp Gly Lys His Glu Cys Leu
 370 375 380
 aac ttg gaa aat ctg gat tgt tgc gtg gtg gga aga gag agc cca ccc 1259
 Asn Leu Glu Asn Leu Asp Cys Cys Val Val Gly Arg Glu Ser Pro Pro
 385 390 395 400
 tct tct tct tca cca ttg tct tgc tta tct act gac tct gct tca tca 1307
 Ser Ser Ser Ser Pro Leu Ser Cys Leu Ser Thr Asp Ser Ala Ser Ser
 405 410 415
 aca aca aca aca aca acc tcg gtt tct tgt aac tat ttg gtc 1349
 Thr Thr Thr Thr Thr Ser Val Ser Cys Asn Tyr Leu Val
 420 425 430
 tgagagagag agctttgcct tctagtttga atttctattt cttccgcttc tttctttttt 1409
 tttctttttt ttgggttctg cttagggttt gtatttcagt ttcagggtt gttcgttggt 1469
 tctgaataat caatgtcttt gccctttttn naangntnca agntnaaana aaaaaaaaaa 1529
 a 1530

<210> 34

<211> 430

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G979

<400> 34

Met Lys Lys Arg Leu Thr Thr Ser Thr Cys Ser Ser Ser Pro Ser Ser
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 20 25 30

Pro Arg Pro Lys Arg Ala Lys Arg Ala Lys Lys Ser Ser Pro Ser Gly
 35 40 45

Asp Lys Ser His Asn Pro Thr Ser Pro Ala Ser Thr Arg Arg Ser Ser
 50 55 60

Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Phe Glu Ala
 65 70 75 80

His Leu Trp Asp Lys Ser Ser Trp Asn Ser Ile Gln Asn Lys Lys Gly
 85 90 95

Lys Gln Val Tyr Leu Gly Ala Tyr Asp Ser Glu Glu Ala Ala Ala His
 100 105 110

Thr Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Asp Thr Ile Leu
 115 120 125

Asn Phe Pro Ala Glu Thr Tyr Thr Lys Glu Leu Glu Glu Met Gln Arg
 130 135 140

Val Thr Lys Glu Glu Tyr Leu Ala Ser Leu Arg Arg Gln Ser Ser Gly
 145 150 155 160

Phe Ser Arg Gly Val Ser Lys Tyr Arg Gly Val Ala Arg His His His
 165 170 175

Asn Gly Arg Trp Glu Ala Arg Ile Gly Arg Val Phe Gly Asn Lys Tyr
 180 185 190

Leu Tyr Leu Gly Thr Tyr Asn Thr Gln Glu Glu Ala Ala Ala Tyr
 195 200 205

Asp Met Ala Ala Ile Glu Tyr Arg Gly Ala Asn Ala Val Thr Asn Phe
 210 215 220

Asp Ile Ser Asn Tyr Ile Asp Arg Leu Lys Lys Lys Gly Val Phe Pro
 225 230 235 240

Phe Pro Val Asn Gln Ala Asn His Gln Glu Gly Ile Leu Val Glu Ala
 245 250 255

Lys Gln Glu Val Glu Thr Arg Glu Ala Lys Glu Glu Pro Arg Glu Glu
 260 265 270

Val Lys Gln Gln Tyr Val Glu Glu Pro Pro Gln Glu Glu Glu Lys
 275 280 285

tca cgt aag ctt cct tcg tcg aaa tat aaa ggc gtt gtg cct cag cct 242
Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro
65 70 75

aac gga aga tgg gga gct cag att tac gag aag cat cag cga gtt tgg	290
Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp	
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ctc ggt act ttc aac gag gaa gaa gaa gct gcg tct tct tac gac atc	338
Leu Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile	
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Ala Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser	
115 120 125	
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Gln Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser	
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aaa gct gag atc gtg gat atg ttg agg aaa cac act tac gcc gat gag	482
Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu	
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ttt gag cag agt aga cgg aag ttt gtt aac gcc gac gga aaa cgc tct	530
Phe Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser	
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Gly Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg	
180 185 190	
gag gtt ttg ttc gag aag act gtt acg ccg agc gac gtc ggg aag ctg	626
Glu Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu	
195 200 205	
aac cgt tta gtg ata ccg aaa caa cac gcg gag aag cat ttt ccg tta	674
Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu	
210 215 220	
ccg gcg atg acg acg gcg atg ggg atg aat ccg tct ccg acg aaa ggc	722
Pro Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly	
225 230 235	
gtt ttg att aac ttg gaa gat aga aca ggg aaa gtg tgg cgg ttc cgt	770
Val Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg	
240 245 250 255	
tac agt tac tgg aac agc agt caa agt tac gtg ttg acc aag gcc tgg	818
Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp	
260 265 270	
agc cgg ttc gtt aaa gag aag aat ctt cga gcc ggt gat gtg gtt tgt	866
Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys	
275 280 285	
ttc gag aga tca acc gga cca gac cgg caa ttg tat atc cac tgg aaa	914
Phe Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys	
290 295 300	

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Val	Arg	Ser	Ser	Pro	Val	Gln	Thr	Val	Val	Arg	Leu	Phe	Gly	Val	Asn	
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Ile	Phe	Asn	Val	Ser	Asn	Glu	Lys	Pro	Asn	Asp	Val	Ala	Val	Glu	Cys	
320 325 330 335																
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Val	Gly	Lys	Lys	Arg	Ser	Arg	Glu	Asp	Asp	Leu	Phe	Ser	Leu	Gly	Cys	
340 345 350																
tcc	aag	aag	cag	gcg	att	atc	aac	atc	ttg	tgacaaattc	tttttttttt					1108
Ser	Lys	Lys	Gln	Ala	Ile	Ile	Asn	Ile	Leu							
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Arg	Lys	Leu	Pro	Ser	Ser	Lys	Tyr	Lys	Gly	Val	Val	Pro	Gln	Pro	Asn	
65 70 75 80																
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Gly	Thr	Phe	Asn	Glu	Glu	Glu	Glu	Ala	Ala	Ser	Ser	Tyr	Asp	Ile	Ala	
100 105 110																
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115 120 125																
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130 135 140																

Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Phe
 145 150 155 160

Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser Gly
 165 170 175

Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg Glu
 180 185 190

Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn
 195 200 205

Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Pro
 210 215 220

Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly Val
 225 230 235 240

Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg Tyr
 245 250 255

Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser
 260 265 270

Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys Phe
 275 280 285

Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys Val
 290 295 300

Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn Ile
 305 310 315 320

Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys Val
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Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys Ser
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Lys Lys Gln Ala Ile Ile Asn Ile Leu
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 <223> G1020

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ctaattacac c atg ccc aac atc acc atg ggt ttg aaa ccc gac ccg gtt 170
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1 5 10

gct cca acg aac ccg act cat cat gag agt aat gct gcc aaa gag att 218
Ala Pro Thr Asn Pro Thr His His Glu Ser Asn Ala Ala Lys Glu Ile
15 20 25

cgt tac aga ggc gtt agg aaa cgt cca tgg gga aga tac gcc gct gag 266
Arg Tyr Arg Gly Val Arg Lys Arg Pro Trp Gly Arg Tyr Ala Ala Glu
30 35 40 45

atc cga gat ccg gtt aag aaa act cga gtc tgg ctc ggt acg ttc gac 314
Ile Arg Asp Pro Val Lys Lys Thr Arg Val Trp Leu Gly Thr Phe Asp
50 55 60

acc gct cag cag gcg gcg cgt gct tac gac gca gcc gcg cgt gac ttt 362
Thr Ala Gln Gln Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Asp Phe
65 70 75

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Arg Gly Val Lys Ala Lys Thr Asn Phe Gly Val Ile Val Gly Ser Ser
80 85 90

cct act cag agt agc acc gtc gtc gac tct ccc acg gcg gca cgg ttt 458
Pro Thr Gln Ser Ser Thr Val Val Asp Ser Pro Thr Ala Ala Arg Phe
95 100 105

ata aca cct ccg cac ctc gag ctc agc tta ggc ggc ggc ggc gct 506
Ile Thr Pro Pro His Leu Glu Leu Ser Leu Gly Gly Gly Ala Cys
110 115 120 125

cgt cgt aag atc ccg ctt gtg cat ccg gtt tac tac tat aac atg gcg 554
Arg Arg Lys Ile Pro Leu Val His Pro Val Tyr Tyr Tyr Asn Met Ala
130 135 140

acg tat cca aag atg acg acg tgt ggt gtc cag agc gag tct gaa acg 602
Thr Tyr Pro Lys Met Thr Thr Cys Gly Val Gln Ser Glu Ser Glu Thr
145 150 155

tcg tcg gtc gtt gat ttc gaa ggt gga gct ggg aag ata tct ccg ccg 650
Ser Ser Val Val Asp Phe Glu Gly Gly Ala Gly Lys Ile Ser Pro Pro
160 165 170

tta gat ctg gat ctt aac tta gct cct ccg gcg gaa taggcctga 696
Leu Asp Leu Asp Leu Asn Leu Ala Pro Pro Ala Glu
175 180 185

gttttttttt tcttatgtcg tttcttttaga caaaaaaaaaa taacgtttcc tttttttttc 756

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Gly Val Arg Lys Arg Pro Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp
 35 40 45

Pro Val Lys Lys Thr Arg Val Trp Leu Gly Thr Phe Asp Thr Ala Gln
 50 55 60

Gln Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Asp Phe Arg Gly Val
 65 70 75 80

Lys Ala Lys Thr Asn Phe Gly Val Ile Val Gly Ser Ser Pro Thr Gln
 85 90 95

Ser Ser Thr Val Val Asp Ser Pro Thr Ala Ala Arg Phe Ile Thr Pro
 100 105 110

Pro His Leu Glu Leu Ser Leu Gly Gly Gly Ala Cys Arg Arg Lys
 115 120 125

Ile Pro Leu Val His Pro Val Tyr Tyr Tyr Asn Met Ala Thr Tyr Pro
 130 135 140

Lys Met Thr Thr Cys Gly Val Gln Ser Glu Ser Glu Thr Ser Ser Val
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Val Asp Phe Glu Gly Gly Ala Gly Lys Ile Ser Pro Pro Leu Asp Leu
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Asp Leu Asn Leu Ala Pro Pro Ala Glu
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<223> G1023

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 may be A, T, C, G, other or unknown

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cttgtttctgg	ggtaaaggac	ttttcttggt	cttgagagag	ttcattttga	ggctttttctg	180
ggaattttga	gagggttttt	agggttttaag	ggggtttggt	tttgaatttc	gcacaccaag	240
tgttcgataa	a atg gct gaa cga aag aaa cgc tct tct att caa acc aat	290				
	Met Ala Glu Arg Lys Lys Arg Ser Ser Ile Gln Thr Asn					
	1 5 10					
aaa ccc aac aaa aaa ccc atg aag aag aaa cct ttt cag cta aat cac	338					
Lys Pro Asn Lys Lys Pro Met Lys Lys Lys Pro Phe Gln Leu Asn His						
	15 20 25					
ctc cca ggt tta tct gaa gat ttg aag act atg aga aaa ctc cgt ttc	386					
Leu Pro Gly Leu Ser Glu Asp Leu Lys Thr Met Arg Lys Leu Arg Phe						
	30 35 40 45					
ggt gtg aat gat cct tac gct act gac tac tca tca agc gaa gaa gaa	434					
Val Val Asn Asp Pro Tyr Ala Thr Asp Tyr Ser Ser Ser Glu Glu Glu						
	50 55 60					
gaa agg agt cag aga agg aaa cgt tat gtc tgt gag atc gat ctt cct	482					
Glu Arg Ser Gln Arg Arg Lys Arg Tyr Val Cys Glu Ile Asp Leu Pro						
	65 70 75					
ttc gct caa gct gct act caa gca gaa tct gaa agc tca tat tgt cag	530					
Phe Ala Gln Ala Ala Thr Gln Ala Glu Ser Glu Ser Tyr Cys Gln						
	80 85 90					
gag agt aac aat aat ggt gta agc aag act aaa atc tca gct tgt agc	578					
Glu Ser Asn Asn Asn Gly Val Ser Lys Thr Lys Ile Ser Ala Cys Ser						
	95 100 105					
aaa aag gtt tta cgc agc aaa gca tct ccg gtc gtt gga cgt tct tct	626					
Lys Lys Val Leu Arg Ser Lys Ala Ser Pro Val Val Gly Arg Ser Ser						
	110 115 120 125					
act act gtc tcg aag cct gtt ggt gtt agg cag agg aaa tgg ggt aaa	674					
Thr Thr Val Ser Lys Pro Val Gly Val Arg Gln Arg Lys Trp Gly Lys						
	130 135 140					
tgg gct gct gag att aga cat cca atc acc aaa gta aga act tgg ttg	722					
Trp Ala Ala Glu Ile Arg His Pro Ile Thr Lys Val Arg Thr Trp Leu						
	145 150 155					
ggt act tac gag acg ctt gaa gaa gca gct gat gct tat gct acc aag	770					
Gly Thr Tyr Glu Thr Leu Glu Gln Ala Ala Asp Ala Tyr Ala Thr Lys						
	160 165 170					
aag ctt gag ttt gat gct ctg gct gca gcc act tct gct gct tcc tct	818					
Lys Leu Glu Phe Asp Ala Leu Ala Ala Thr Ser Ala Ala Ser Ser						
	175 180 185					
gtt ttg tca aat gag tct ggt tct atg atc tca gcc tca ggg tca agc	866					
Val Leu Ser Asn Glu Ser Gly Ser Met Ile Ser Ala Ser Gly Ser Ser						
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 35 40 45

Asp Pro Tyr Ala Thr Asp Tyr Ser Ser Ser Glu Glu Glu Glu Arg Ser
 50 55 60

Gln Arg Arg Lys Arg Tyr Val Cys Glu Ile Asp Leu Pro Phe Ala Gln
 65 70 75 80

Ala Ala Thr Gln Ala Glu Ser Glu Ser Ser Tyr Cys Gln Glu Ser Asn
 85 90 95

Asn Asn Gly Val Ser Lys Thr Lys Ile Ser Ala Cys Ser Lys Lys Val
 100 105 110

Leu Arg Ser Lys Ala Ser Pro Val Val Gly Arg Ser Ser Thr Thr Val
 115 120 125

Ser Lys Pro Val Gly Val Arg Gln Arg Lys Trp Gly Lys Trp Ala Ala
 130 135 140

Glu Ile Arg His Pro Ile Thr Lys Val Arg Thr Trp Leu Gly Thr Tyr
 145 150 155 160

Glu Thr Leu Glu Gln Ala Ala Asp Ala Tyr Ala Thr Lys Lys Leu Glu
 165 170 175

Phe Asp Ala Leu Ala Ala Ala Thr Ser Ala Ala Ser Ser Val Leu Ser
 180 185 190

Asn Glu Ser Gly Ser Met Ile Ser Ala Ser Gly Ser Ser Ile Asp Leu
 195 200 205

Asp Lys Lys Leu Val Asp Ser Thr Leu Asp Gln Gln Ala Gly Glu Ser
 210 215 220

Lys Lys Ala Ser Phe Asp Phe Asp Phe Ala Asp Leu Gln Ile Pro Glu
 225 230 235 240

Met Gly Cys Phe Ile Asp Asp Ser Phe Ile Pro Asn Ala Cys Glu Leu
 245 250 255

Asp Phe Leu Leu Thr Glu Glu Asn Asn Asn Gln Met Leu Asp Asp Tyr
 260 265 270

Cys Gly Ile Asp Asp Leu Asp Ile Ile Gly Leu Glu Cys Asp Gly Pro
 275 280 285

Ser Glu Leu Pro Asp Tyr Asp Phe Ser Asp Val Glu Ile Asp Leu Gly
 290 295 300

Leu Ile Gly Thr Thr Ile Asp Lys Tyr Ala Phe Val Asp His Ile Ala
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gacaattata acagtataga gaaggaagaa agaaaagaaa aagaaaccgt tgttgattta 180
gatacagaga agagaagatc atctaac atg gga aga tct cct atc tct gat gac 234
Met Gly Arg Ser Pro Ile Ser Asp Asp
1 5
tct ggt ctc aag aaa ggt cct tgg act cct gat gaa gat gag aaa ctt 282
Ser Gly Leu Lys Lys Gly Pro Trp Thr Pro Asp Glu Asp Glu Lys Leu
10 15 20 25
gtc aac tat gtt caa aaa cat ggt cat agt agc tgg aga gcc ctt ccc 330
Val Asn Tyr Val Gln Lys His Gly His Ser Ser Trp Arg Ala Leu Pro
30 35 40
aaa ctc gct ggt ctt aac agg tgt ggg aag agt tgc agg cta aga tgg 378
Lys Leu Ala Gly Leu Asn Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp
45 50 55
acg aac tac ttg aga cca gac atc aag aga ggg aga ttc tct ccg gac 426
Thr Asn Tyr Leu Arg Pro Asp Ile Lys Arg Gly Arg Phe Ser Pro Asp
60 65 70
gag gaa cag act atc ttg aat ctt cat tca gtt ctt gga aac aag tgg 474
Glu Glu Gln Thr Ile Leu Asn Leu His Ser Val Leu Gly Asn Lys Trp
75 80 85
tca acg att gcg aat cag tta cca ggg aga aca gat aac gag atc aag 522
Ser Thr Ile Ala Asn Gln Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys
90 95 100 105
aat ttc tgg aac act cat ttg aag aag aag ctg att cag atg ggt ttt 570
Asn Phe Trp Asn Thr His Leu Lys Lys Lys Leu Ile Gln Met Gly Phe
110 115 120

[illegible]

1441

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Gly	His	Ser	Ser	Trp	Arg	Ala	Leu	Pro	Lys	Leu	Ala	Gly	Leu	Asn	Arg
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Cys	Gly	Lys	Ser	Cys	Arg	Leu	Arg	Trp	Thr	Asn	Tyr	Leu	Arg	Pro	Asp
	50					55						60			
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Leu	His	Ser	Val	Leu	Gly	Asn	Lys	Trp	Ser	Thr	Ile	Ala	Asn	Gln	Leu
				85					90					95	
Pro	Gly	Arg	Thr	Asp	Asn	Glu	Ile	Lys	Asn	Phe	Trp	Asn	Thr	His	Leu
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Lys	Lys	Lys	Leu	Ile	Gln	Met	Gly	Phe	Asp	Pro	Met	Thr	His	Arg	Pro
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Asn	Leu	Arg	Gly	Phe	Val	Asp	Leu	Gln	Gln	Gln	Phe	Pro	Ile	Asp	Gln
					150					155					160
Glu	His	Thr	Ile	Leu	Lys	Leu	Gln	Thr	Glu	Met	Ala	Lys	Leu	Gln	Leu
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Phe	Gln	Tyr	Leu	Leu	Gln	Pro	Ser	Ser	Met	Ser	Asn	Asn	Val	Asn	Pro
			180					185					190		
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	210					215					220				

Gly Ser Tyr Leu Gln Asp Phe His Ser Leu Pro Ser Leu Lys Thr Leu
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245 250 255

Asn His Phe Lys Phe Ser Thr Gln Arg Glu Asn Leu Pro Val Ser Pro
260 265 270

Ile Trp Leu Ser Asp Pro Ser Ser Thr Thr Pro Ala His Val Asn Asp
275 280 285

Asp Leu Ile Phe Asn Gln Tyr Gly Ile Glu Asp Val Asn Ser Asn Ile
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<222> (96)..(842)
<223> G663

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Met Glu Gly Ser Ser Lys
1 5

ggg ttg agg aaa ggt gca tgg act gct gaa gaa gat agt etc ttg agg 161
Gly Leu Arg Lys Gly Ala Trp Thr Ala Glu Glu Asp Ser Leu Leu Arg
10 15 20

cta tgt att gat aag tat gga gaa ggc aaa tgg cat caa gtt cct ttg 209
Leu Cys Ile Asp Lys Tyr Gly Glu Gly Lys Trp His Gln Val Pro Leu
25 30 35

aga gct ggg cta aat cga tgc aga aag agt tgt aga cta aga tgg ttg 257
Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser Cys Arg Leu Arg Trp Leu
40 45 50

aac tat ttg aag cca agt atc aag aga gga aga ctt agc aat gat gaa 305
Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly Arg Leu Ser Asn Asp Glu
55 60 65 70

gtt gat ctt ctt ctt cgc ctt cat aag ctt cta gga aat agg tgg tcc 353
Val Asp Leu Leu Leu Arg Leu His Lys Leu Gly Asn Arg Trp Ser
75 80 85

0030459-001300

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 90 95 100
 tac tgg aac acc cat ctg agt aaa aaa cat gag tct tcg tgt tgt aag 449
 Tyr Trp Asn Thr His Leu Ser Lys Lys His Glu Ser Ser Cys Cys Lys
 105 110 115
 tct aaa atg aaa aag aaa aac att att tcc cct cct aca aca cgg gtc 497
 Ser Lys Met Lys Lys Lys Asn Ile Ile Ser Pro Pro Thr Thr Pro Val
 120 125 130
 caa aaa atc ggt gtt ttt aag cct cga cct cga tcc ttc tct gtt aac 545
 Gln Lys Ile Gly Val Phe Lys Pro Arg Pro Arg Ser Phe Ser Val Asn
 135 140 145 150
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 155 160 165
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 Ser Cys Leu Gly Leu Lys Lys Asn Asn Val Cys Glu Asn Ser Ile Thr
 170 175 180
 tgt aac aaa gat gat gag aaa gat gat ttt gtg aat aat cta atg aat 689
 Cys Asn Lys Asp Asp Glu Lys Asp Asp Phe Val Asn Asn Leu Met Asn
 185 190 195
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 Gly Asp Asn Met Trp Leu Glu Asn Leu Leu Gly Glu Asn Gln Glu Ala
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 Asp Ala Ile Val Pro Glu Ala Thr Thr Ala Glu His Gly Ala Thr Leu
 215 220 225 230
 gcg ttt gac gtt gag caa ctt tgg agt ctg ttt gat gga gag act gtt 833
 Ala Phe Asp Val Glu Gln Leu Trp Ser Leu Phe Asp Gly Glu Thr Val
 235 240 245
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Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly
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Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys Leu His Ser Leu
70 75 80

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Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
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gat aac gag ata aag aac tat tgg aac acg cat ata cga aga aag ctt 451
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ata aac aga ggg att gat cca acg agt cat aga cca atc caa gaa tca 499
Ile Asn Arg Gly Ile Asp Pro Thr Ser His Arg Pro Ile Gln Glu Ser
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Ser Ala Ser Gln Asp Ser Lys Pro Thr Gln Leu Glu Pro Val Thr Ser
135 140 145

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165 170 175 180

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Met Thr Arg Arg Cys Ser His Cys Asn His Asn Gly His Asn Ser
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Arg Thr Cys Pro Asn Arg Gly Val Lys Leu Phe Gly Val Arg Leu Thr
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 Ser Phe Pro Ile Leu Tyr Pro Thr Tyr Phe Ser Pro Tyr Tyr Pro Phe
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 275 280 285
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 305 310 315 320
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Ala Glu Thr Ser Thr Asp Ala Thr Glu Thr Thr Ile Ala Thr Thr Glu

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Ala Gly Glu Ala Pro Glu Lys Lys Val Arg Lys Ala Tyr Thr Ile Thr

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Lys Ser Arg Glu Ser Trp Thr Glu Gly Glu His Asp Lys Phe Leu Glu

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Ala Leu Gln Leu Phe Asp Arg Asp Trp Lys Lys Ile Glu Asp Phe Val

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95 100 105

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Pro Lys Arg Lys Ala Ala His Pro Tyr Pro Gln Lys Ala Ser Lys Asn

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Ala Gln Met Ser Leu His Val Ser Met Ser Phe Pro Thr Gln Ile Asn

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Asn Leu Pro Gly Tyr Thr Pro Trp Asp Asp Asp Thr Ser Ala Leu Leu

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Asn Ile Ala Val Ser Gly Val Ile Pro Pro Glu Asp Glu Leu Asp Thr

160 165 170

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175 180 185

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Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro
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gac atc aaa aga gga aag ttt tca gcc gaa gaa gag caa aca atc ctc 239
Asp Ile Lys Arg Gly Lys Phe Ser Ala Glu Glu Gln Thr Ile Leu
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His Leu His Ser Ile Leu Gly Asn Lys Trp Ser Ala Ile Ala Thr His
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cta aag aag aaa ttg atc cag atg ggg atc gat cct gtg act cat cag 383
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115 120 125

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Gly Glu Ala Ala Gln Leu Ala Asn Leu Gln Tyr Leu Gln Arg Met Phe
160 165 170 175

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180 185 190

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Thr Glu Met Ala Met Glu Gln Asp Pro Thr Gln Glu Asn Ser Pro Leu	
175 180 185	
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 Gln Lys Tyr Phe Leu Arg Arg Thr Asn Leu Asn Arg Arg Arg Arg
 145 150 155 160
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 tctctctgct cataccacaa accggttccat tcttccccta atcacaaagt gatatttaca 180
 tagagaagat agag atg gga aga cca cca tgc tgt gac aag att gga gtg 230
 Met Gly Arg Pro Pro Cys Cys Asp Lys Ile Gly Val
 1 5 10
 aag aaa gga cca tgg aca cca gag gaa gat atc atc ttg gtt tct tac 278
 Lys Lys Gly Pro Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr
 15 20 25
 atc caa gaa cat ggt cct gga aac tgg aga tct gtg cct act cac aca 326
 Ile Gln Glu His Gly Pro Gly Asn Trp Arg Ser Val Pro Thr His Thr
 30 35 40
 ggt ttg agg aga tgt agc aaa agc tgt aga ttg agg tgg act aat tat 374
 Gly Leu Arg Arg Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr
 45 50 55 60

ctt	cga	cct	ggg	atc	aag	cgt	gga	aat	ttc	acc	gag	cat	gaa	gag	aag	422
Leu	Arg	Pro	Gly	Ile	Lys	Arg	Gly	Asn	Phe	Thr	Glu	His	Glu	Glu	Lys	
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atg	att	ctc	cat	ctt	caa	gct	ctt	ttg	gga	aac	agg	tgg	gca	gct	ata	470
Met	Ile	Leu	His	Leu	Gln	Ala	Leu	Leu	Gly	Asn	Arg	Trp	Ala	Ala	Ile	
			80						85							
gca	tca	tat	ctt	cca	gaa	agg	aca	gac	aat	gat	ata	aag	aac	tat	tgg	518
Ala	Ser	Tyr	Leu	Pro	Glu	Arg	Thr	Asp	Asn	Asp	Ile	Lys	Asn	Tyr	Trp	
		95						100					105			
aac	act	cat	ttg	aag	aaa	aag	ctc	aag	aag	atg	aat	gat	tct	tgt	gat	566
Asn	Thr	His	Leu	Lys	Lys	Lys	Leu	Lys	Lys	Met	Asn	Asp	Ser	Cys	Asp	
			110									120				
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Ser	Thr	Ile	Asn	Asn	Gly	Leu	Asp	Asn	Lys	Asp	Phe	Ser	Ile	Ser	Asn	
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Lys	Asn	Thr	Thr	Ser	His	Gln	Ser	Ser	Asn	Ser	Ser	Lys	Gly	Gln	Trp	
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Glu	Arg	Arg	Leu	Gln	Thr	Asp	Ile	Asn	Met	Ala	Lys	Gln	Ala	Leu	Cys	
			160						165							
gat	gcc	ttg	tct	att	gac	aaa	cca	caa	aac	cca	act	aat	ttt	tct	att	758
Asp	Ala	Leu	Ser	Ile	Asp	Lys	Pro	Gln	Asn	Pro	Thr	Thr	Asn	Phe	Ser	
			175						180					185		
ccc	gat	ctt	ggt	tat	ggt	cca	tca	tct	tct	tcg	tcc	tct	acc	acc	acc	806
Pro	Asp	Leu	Gly	Tyr	Gly	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Thr	Thr	Thr	
			190									200				
acc	acc	acc	acc	acc	acc	acg	aga	aac	act	aat	cca	tac	cca	tct	ggg	854
Thr	Thr	Thr	Thr	Thr	Thr	Thr	Arg	Asn	Thr	Asn	Pro	Tyr	Pro	Ser	Gly	
											215				220	
gtc	tat	gct	tca	agt	gct	gag	aac	att	gct	cgt	ttg	ctt	cag	aat	ttt	902
Val	Tyr	Ala	Ser	Ser	Ala	Glu	Asn	Ile	Ala	Ala	Leu	Leu	Gln	Asn	Phe	
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atg	aaa	gac	aca	cca	aag	acc	tcg	gtg	ccc	ttg	ccg	gtt	gca	gcc	acc	950
Met	Lys	Asp	Thr	Pro	Lys	Thr	Ser	Val	Pro	Leu	Pro	Val	Ala	Ala	Thr	
			240						245					250		
gag	atg	gct	atc	acc	acg	gca	gct	tcg	agc	cct	agc	aca	acc	gaa	gga	998
Glu	Met	Ala	Ile	Thr	Thr	Ala	Ala	Ser	Ser	Pro	Ser	Thr	Thr	Glu	Gly	

gaa gct gaa gag aag cct aaa cta ata gac cat gac att aat ggt cta 1094
 Glu Ala Glu Glu Lys Pro Lys Leu Ile Asp His Asp Ile Asn Gly Leu
 285 290 295 300

att aca caa ggc tct ctt tct ttg ttc gag aaa tgg ctc ttt gat gag 1142
 Ile Thr Gln Gly Ser Leu Ser Leu Phe Glu Lys Trp Leu Phe Asp Glu
 305 310 315

caa agc cac gat atg atc atc aat aac atg tca cta gag ggt cag gaa 1190
 Gln Ser His Asp Met Ile Ile Asn Asn Met Ser Leu Glu Gly Gln Glu
 320 325 330

gtg ttg ttc tagaaagcat taaagttga cgatttgctt gaggaaccac 1239
 Val Leu Phe
 335

gaggcttagt tataaacaat ttgtataatt aagtactctt tagttttgtt ttcaatcctt 1299

attatgatca tattgcagta attagggatt ttagtcttta gtagtaactc ttaagtttta 1359

acacattttt ctctatcttt ttagtagtaa ctcttttatt tttccttaaa tctttgtcga 1419

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taacgtcttt ttaaaaaaaaa aaaaaaaaaa a 1510

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<212> PRT

<213> Arabidopsis thaliana

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<223> G932

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 35 40 45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
 50 55 60

Ile Lys Arg Gly Asn Phe Thr Glu His Glu Glu Lys Met Ile Leu His
 65 70 75 80

Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu
 85 90 95

Pro Glu Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr His Leu
 100 105 110


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Lys Lys Lys Leu Lys Lys Met Asn Asp Ser Cys Asp Ser Thr Ile Asn
115                               120

Asn Gly Leu Asp Asn Lys Asp Phe Ser Ile Ser Asn Lys Asn Thr Thr
130                               135                               140

Ser His Gln Ser Ser Asn Ser Ser Lys Gly Gln Trp Glu Arg Arg Leu
145                               150                               155                               160

Gln Thr Asp Ile Asn Met Ala Lys Gln Ala Leu Cys Asp Ala Leu Ser
165                               170                               175

Ile Asp Lys Pro Gln Asn Pro Thr Asn Phe Ser Ile Pro Asp Leu Gly
180                               185                               190

Tyr Gly Pro Ser Ser Ser Ser Ser Ser Thr Thr Thr Thr Thr Thr Thr
195                               200                               205

Thr Thr Thr Arg Asn Thr Asn Pro Tyr Pro Ser Gly Val Tyr Ala Ser
210                               215                               220

Ser Ala Glu Asn Ile Ala Arg Leu Leu Gln Asn Phe Met Lys Asp Thr
225                               230                               235                               240

Pro Lys Thr Ser Val Pro Leu Pro Val Ala Ala Thr Glu Met Ala Ile
245                               250                               255

Thr Thr Ala Ala Ser Ser Pro Ser Thr Thr Glu Gly Asp Gly Glu Gly
260                               265                               270

Ile Asp His Ser Leu Phe Ser Phe Asn Ser Ile Asp Glu Ala Glu Glu
275                               280                               285

Lys Pro Lys Leu Ile Asp His Asp Ile Asn Gly Leu Ile Thr Gln Gly
290                               295                               300

Ser Leu Ser Leu Phe Glu Lys Trp Leu Phe Asp Glu Gln Ser His Asp
305                               310                               315                               320

Met Ile Ile Asn Asn Met Ser Leu Glu Gly Gln Glu Val Leu Phe
325                               330                               335

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<210> 59
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<212> DNA
<213> Arabidopsis thaliana

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<220>
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<222> (180)..(914)
<223> G994

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<220>
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      may be A, T, C, G, other or unknown

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 Thr Met Leu Leu Ser Gly Asp Ile Thr Ser Ser Cys Ser Ser Ser Ser
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tct ttg tgg atg aag tat gga gaa ttc gga tac gaa gat tta gaa ctt 899
 Ser Leu Trp Met Lys Tyr Gly Glu Phe Gly Tyr Glu Asp Leu Glu Leu
 225 230 235 240

gga tgt ttc gat gtt tagagattca agtatgttta attagggcgt aggttgatta 954
 Gly Cys Phe Asp Val
 245

atcataaggt tcattgactt cattctagaa ttgtgtagtt ggaccagtat aaagaatcaa 1014

agttangaaa cattgtaatt tgatttccaa attaactctan tgaataaatg tgctttgcaa 1074

aaaaaaaaa aaaaaaaaaa a 1095

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 <213> Arabidopsis thaliana

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 <223> G994

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Arg Gly Asn Cys Gly Gly Gly Gly Gly Gly Trp Cys Trp Arg Asp Val
 35 40 45

Pro Lys Leu Ala Gly Leu Arg Arg Cys Gly Lys Ser Cys Arg Leu Arg
 50 55 60

Trp Thr Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly Leu Phe Thr Glu
 65 70 75 80

Glu Glu Ile Gln Leu Val Ile Asp Leu His Ala Arg Leu Gly Asn Arg
 85 90 95

Trp Ser Lys Ile Ala Val Glu Leu Pro Gly Arg Thr Asp Asn Asp Ile
 100 105 110

Lys Asn Tyr Trp Asn Thr His Ile Lys Arg Lys Leu Ile Arg Met Gly
 115 120 125

Ile Asp Pro Asn Thr His Arg Arg Phe Asp Gln Gln Lys Val Asn Glu
 130 135 140

Glu Glu Thr Ile Leu Val Asn Asp Pro Lys Pro Leu Ser Glu Thr Glu
 145 150 155 160

Val Ser Val Ala Leu Lys Asn Asp Thr Ser Ala Val Leu Ser Gly Asn
 165 170
 Leu Asn Gln Leu Ala Asp Val Asp Gly Asp Asp Gln Pro Trp Ser Phe
 180 185 190
 Leu Met Glu Asn Asp Glu Gly Gly Gly Gly Asp Ala Ala Gly Glu Leu
 195 200 205
 Thr Met Leu Leu Ser Gly Asp Ile Thr Ser Ser Cys Ser Ser Ser Ser
 210 215 220
 Ser Leu Trp Met Lys Tyr Gly Glu Phe Gly Tyr Glu Asp Leu Glu Leu
 225 230 235 240
 Gly Cys Phe Asp Val
 245

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 <223> G996

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 atg gga aga cat tca tgt tgt tac aaa cag aaa ctg agg aaa gga ctt 166
 Met Gly Arg His Ser Cys Cys Tyr Lys Gln Lys Leu Arg Lys Gly Leu
 1 5 10 15
 tgg tct cct gaa gaa gat gag aag ctt ctt cgt tac atc act aag tat 214
 Trp Ser Pro Glu Glu Asp Glu Lys Leu Leu Arg Tyr Ile Thr Lys Tyr
 20 25 30
 ggt cat ggt tgc tgg agc tct gtc cct aaa caa gct ggt tta cag aga 262
 Gly His Gly Cys Trp Ser Ser Val Pro Lys Gln Ala Gly Leu Gln Arg
 35 40 45
 tgt gga aaa agt tgt aga tta aga tgg ata aat tat tta aga cca gat 310
 Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60
 ttg aag aga gga gca ttt tct caa gat gaa gaa aat ctc att att gaa 358
 Leu Lys Arg Gly Ala Phe Ser Gln Asp Glu Glu Asn Leu Ile Ile Glu
 65 70 75 80
 ctt cat gcc gtt ctt ggc aat aga tgg tct cag ata gct gca cag ctt 406
 Leu His Ala Val Leu Gly Asn Arg Trp Ser Gln Ile Ala Ala Gln Leu
 85 90 95

1126

1148

His His His His Val Asp Glu Thr Ile Pro Ser Ala Val Val Leu Pro
210 215 220

Gly Ser Met Phe Ser Ser Gly Leu Thr Gly Tyr Arg Ser Ser Asn Leu
225 230 235 240

Gly Leu Ile Glu Leu Glu Asn Ser Phe Ser Thr Gly Pro Met Met Thr
245 250 255

Glu His Gln Gln Ile Gln Glu Ser Asn Tyr Asn Asn Ser Thr Phe Phe
260 265 270

Gly Asn Gly Asn Leu Asn Trp Gly Leu Thr Met Glu Glu Asn Gln Asn
275 280 285

Pro Phe Thr Ile Ser Asn His Ser Asn Ser Ser Leu Tyr Ser Asp Ile
290 295 300

Lys Ser Glu Thr Asn Phe Phe Gly Thr Glu Ala Thr Asn Val Gly Met
305 310 315 320

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325 330 335

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<223> G997

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Met Ala Ser Ser Ser Met Ser Thr Ser Ser Trp Thr Ala Arg

1

5

10

gag gac aag caa ttc gaa atg gcg ttg gcg aaa ttc gac aag gac act 159
Glu Asp Lys Gln Phe Glu Met Ala Leu Ala Lys Phe Asp Lys Asp Thr
15 20 25 30

cct gac cgt tgg caa aaa att gca agg gca gtt ggt ggg aaa tca act 207
Pro Asp Arg Trp Gln Lys Ile Ala Arg Ala Val Gly Gly Lys Ser Thr
35 40 45

gaa gaa gta aag cga cac tat gaa ttg ctc ctt agg gat gtg aat gac 255
Glu Glu Val Lys Arg His Tyr Glu Leu Leu Leu Arg Asp Val Asn Asp
50 55 60

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ile Glu Ser Gly Arg Tyr Pro Gln Pro Arg Tyr Arg Asn Thr Asn
65 70 75

tgaagccatt aataaaatgc ctttctatca agaagaggac atttgagaga atctataaag 360

aactaagaat ttcatgtgat ttcttatatt ctatttgctt tctttttttt tttttttttt 420

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cga Arg	cca Pro	gat Asp 65	att Ile	aag Lys	cgt Arg	gga Gly	aga Arg 70	ttc Phe	tct Ser	ttt Phe	gaa Glu	gaa Glu 75	gaa Glu	gaa Glu	acc Thr	300
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gct Ala 95	cgt Arg	ttg Leu	cct Pro	gga Gly	aga Arg 100	aca Thr	gac Asp	aac Asn	gag Glu	atc Ile 105	aaa Lys	aac Asn	tat Tyr	tgg Trp	aac Asn 110	396
act Thr	cac His	atc Ile	aga Arg	aaa Lys 115	aga Arg	ctt Leu	cta Leu	aag Lys	atg Met 120	gga Gly	atc Ile	gac Asp	ccg Pro	ggt Val 125	aca Thr	444
cac His	act Thr	cca Pro	cgt Arg 130	ctt Leu	gat Asp	ctt Leu	ctc Leu	gat Asp 135	atc Ile	tcc Ser	tcc Ser	att Ile	ctc Leu 140	agc Ser	tca Ser	492
tct Ser	atc Ile 145	tac Tyr	aac Asn	tct Ser	tcg Ser	cat His	cat His 150	cat His	cat His	cat His	cat His 155	cat His	caa Gln	caa Gln	cat His	540
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gtt Val 175	aac Asn	ccc Pro	gag Glu	ata Ile	ctc Leu 180	aaa Lys	ctc Leu	gca Ala	acc Thr	tct Ser 185	ctc Leu	ttt Phe	tca Ser	aac Asn 190	caa Gln	636
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gta Val	aac Asn	caa Gln	tac Tyr 210	caa Gln	acc Thr	ggg Gly	tac Tyr 215	aac Asn	atg Met	cct Pro	ggg Gly	aat Asn	gaa Glu 220	gaa Glu	tta Leu	732
caa Gln	tct Ser	tgg Trp 225	ttc Phe	cct Pro	atc Ile	atg Met	gat Asp 230	caa Gln	ttc Phe	acg Thr	aat Asn 235	ttc Phe	caa Gln	gac Asp	ctc Leu	780
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 Ser Ser Thr Tyr Ile Asn Ser Ser Thr Cys Ser Thr Glu Asp Glu Lys 300
 290 295

gag agt tat tac agt gat aat atc act aat tat tgc ttt gat gtt aat 1020
 Glu Ser Tyr Tyr Ser Asp Asn Ile Thr Asn Tyr Ser Phe Asp Val Asn 315
 305 310

ggt ttt ctc caa ttc caa taaacaaaac gccattggaa tagagttatg 1068
 Gly Phe Leu Gln Phe Gln 320

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 35 40 45
 Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro
 50 55 60
 Asp Ile Lys Arg Gly Arg Phe Ser Phe Glu Glu Glu Thr Ile Ile
 65 70 75 80
 Gln Leu His Ser Ile Met Gly Asn Lys Trp Ser Ala Ile Ala Ala Arg
 85 90 95
 Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His
 100 105 110
 Ile Arg Lys Arg Leu Leu Lys Met Gly Ile Asp Pro Val Thr His Thr
 115 120 125
 Pro Arg Leu Asp Leu Leu Asp Ile Ser Ser Ile Leu Ser Ser Ser Ile
 130 135 140

00154410-00154410

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 Lys Arg Arg Asn Gly Leu Ile Lys Lys Ala Lys Glu Leu Ser Ile Leu
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tgt gac gcc gag gtt gct ctt atc atc ttc tcc agc acc ggc aag att 260
 Cys Asp Ala Glu Val Ala Leu Ile Ile Phe Ser Ser Thr Gly Lys Ile
 40 45 50

tac gat ttc tcc agc gtc tgt atg gag caa att ctt tct aga tat gga 308
 Tyr Asp Phe Ser Ser Val Cys Met Glu Gln Ile Leu Ser Arg Tyr Gly
 55 60 65 70

tac act act gcg tcc act gag cat aaa caa caa aga gaa cac caa ctt 356
 Tyr Thr Thr Ala Ser Thr Glu His Lys Lys Gln Arg Glu His Gln Leu
 75 80 85

cta att tgt gct tca cat gga aat gaa gct gtg ttg cga aat gat gat 404
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tct atg aag ggg gaa ctt gaa aga tta cag ctt gca att gag aga ctt 452
 Ser Met Lys Gly Glu Leu Glu Arg Leu Gln Leu Ala Ile Glu Arg Leu
 105 110 115

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gaa aac cag ttg aac gag agc ttg cat agt gtc aag gat caa aag aca 548
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 135 140 145 150

caa atc ctg ctc aac cag att gag aga tcc agg ata cag gag aaa aaa 596
 Gln Ile Leu Leu Asn Gln Ile Glu Arg Ser Arg Ile Gln Glu Lys Lys
 155 160 165

gca ttg gaa gaa aac caa atc ttg cgc aaa cag gtt gag atg ttg ggg 644
 Ala Leu Glu Glu Asn Gln Ile Leu Arg Lys Gln Val Glu Met Leu Gly
 170 175 180

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 Arg Gly Ser Gly Pro Lys Val Leu Asn Glu Arg Pro Gln Asp Ser Ser
 185 190 195

cca gaa gcc gat ccc gag agc tct tca tca gaa gag gat gag aat gac 740
 Pro Glu Ala Asp Pro Glu Ser Ser Ser Ser Glu Glu Asp Glu Asn Asp
 200 205 210

aac gag gag cac cat tcc gac act tcc ttg cag ttg ggg ttg tcg tcg 788
 Asn Glu Glu His His Ser Ser Thr Ser Leu Gln Leu Gly Leu Ser Ser
 215 220 225 230

acg ggg tat tgc aca aag aga aag aag ccg aag atc gaa ctg gtc tgc 836
 Thr Gly Tyr Cys Thr Lys Arg Lys Lys Pro Lys Ile Glu Leu Val Cys
 235 240 245

gat aac tct ggg agt caa gtg gct tct gat tgatggaatc gattattttt 886
 Asp Asn Ser Gly Ser Gln Val Ala Ser Asp
 250 255

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 35 40 45
 Ser Ser Thr Gly Lys Ile Tyr Asp Phe Ser Ser Val Cys Met Glu Gln
 50 55 60
 Ile Leu Ser Arg Tyr Gly Tyr Thr Thr Ala Ser Thr Glu His Lys Gln
 65 70 75 80
 Gln Arg Glu His Gln Leu Leu Ile Cys Ala Ser His Gly Asn Glu Ala
 85 90 95
 Val Leu Arg Asn Asp Asp Ser Met Lys Gly Glu Leu Glu Arg Leu Gln
 100 105 110
 Leu Ala Ile Glu Arg Leu Lys Gly Lys Glu Leu Glu Gly Met Ser Phe
 115 120 125
 Pro Asp Leu Ile Ser Leu Glu Asn Gln Leu Asn Glu Ser Leu His Ser
 130 135 140
 Val Lys Asp Gln Lys Thr Gln Ile Leu Leu Asn Gln Ile Glu Arg Ser
 145 150 155 160
 Arg Ile Gln Glu Lys Lys Ala Leu Glu Glu Asn Gln Ile Leu Arg Lys
 165 170 175

Gln Val Glu Met Leu Gly Arg Gly Ser Gly Pro Lys Val Leu Asn Glu
180 185 190

Arg Pro Gln Asp Ser Ser Pro Glu Ala Asp Pro Glu Ser Ser Ser Ser
195 200 205

Glu Glu Asp Glu Asn Asp Asn Glu Glu His His Ser Asp Thr Ser Leu
210 215 220

Gln Leu Gly Leu Ser Ser Thr Gly Tyr Cys Thr Lys Arg Lys Lys Pro
225 230 235 240

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<211> 1210

<212> DNA

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<222> (117)..(836)

<223> G860

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may be A, T, C, G, other or unknown

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Met
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Gly Arg Gly Lys Ile Ala Ile Lys Arg Ile Asn Asn Ser Thr Ser Arg
5 10 15

cag gtt acg ttc tcg aag cga agg aat gga ttg ttg aag aaa gct aag 215
Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala Lys
20 25 30

gag ctt gcg att ctc tgc gat gct gag gtt ggt gtc atc atc ttc tcc 263
Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Val Ile Ile Phe Ser
35 40 45

agc acc ggt agg ctc tac gat ttc tcc agc tcc agc atg aaa tcg gtc 311
Ser Thr Gly Arg Leu Tyr Asp Phe Ser Ser Ser Ser Met Lys Ser Val
50 55 60 65

ata gag aga tac agc gat gcc aaa gga gaa acc agt tca gaa aat gat 359
Ile Glu Arg Tyr Ser Asp Ala Lys Gly Glu Thr Ser Ser Glu Asn Asp
70 75 80

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ccc gct tca gaa att cag ttc tgg caa aag gag gct gcg att cta aag 407
Pro Ala Ser Glu Ile Gln Phe Trp Gln Lys Glu Ala Ala Ile Leu Lys
      85                      90                      95

cgt cag cta cat aac ttg caa gaa aac cac cgg caa atg atg ggg gag 455
Arg Gln Leu His Asn Leu Gln Glu Asn His Arg Gln Met Met Gly Glu
      100                      105                      110

gag ctc tct gga cta agt gta gaa gct tta cag aat ttg gaa aat cag 503
Glu Leu Ser Gly Leu Ser Val Glu Ala Leu Gln Asn Leu Glu Asn Gln
      115                      120                      125

ctt gaa ttg agc ctt cgt ggc gtt cga atg aaa aag gat caa atg tta 551
Leu Glu Leu Ser Leu Arg Gly Val Arg Met Lys Lys Asp Gln Met Leu
      130                      135                      140                      145

atc gaa gaa ata caa gta ctt aac cga gag ggg aat ctc gtt cac caa 599
Ile Glu Glu Ile Gln Val Leu Asn Arg Glu Gly Asn Leu Val His Gln
      150                      155                      160

gag aat tta gac ctc cac aag aaa gta aac cta atg cac caa cag aac 647
Glu Asn Leu Asp Leu His Lys Lys Val Asn Leu Met His Gln Gln Asn
      165                      170                      175

atg gaa cta cat gaa aag gtt tca gag gtc gag ggt gtg aaa atc gca 695
Met Glu Leu His Glu Lys Val Ser Glu Val Glu Gly Val Lys Ile Ala
      180                      185                      190

aac aag aat tct ctt ctc aca aat ggt cta gac atg aga gat acc tcg 743
Asn Lys Asn Ser Leu Leu Thr Asn Gly Leu Asp Met Arg Asp Thr Ser
      195                      200                      205

aac gaa cat gtc cat ctt cag ctc agc caa ccg cag cat gat cat gag 791
Asn Glu His Val His Leu Gln Leu Ser Gln Pro Gln His Asp His Glu
      210                      215                      220                      225

acg cat tca aaa gct atc caa ctc aac tat ttt tcc ttc att gca 836
Thr His Ser Lys Ala Ile Gln Leu Asn Tyr Phe Ser Phe Ile Ala
      230                      235                      240

taatataatt cgggtgtgcc acacacttat gttgacctcg tcggaatcat atcacaattc 896

actgtgtcag cttgcctctg cataagcgaa aataaaaaca taaacatgat cagtttgcat 956

tccatatcta tcaaacacca gctttgtaac ttttaaaact ttttctccgt gcaaagacct 1016

ttgggtttggc gcttaagcat gtagtttgat gatcaaagga aatgggtgtt ttagcataaa 1076

gttgtcaccc ttccgttgca ttttagcttc ccatccaaat caatttgtaa aatgtgagtt 1136

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aaaaaaaaaa aaaa 1210

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 20 25 30

Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Val Ile Ile Phe
 35 40 45

Ser Ser Thr Gly Arg Leu Tyr Asp Phe Ser Ser Ser Met Lys Ser
 50 55 60

Val Ile Glu Arg Tyr Ser Asp Ala Lys Gly Glu Thr Ser Ser Glu Asn
 65 70 75 80

Asp Pro Ala Ser Glu Ile Gln Phe Trp Gln Lys Glu Ala Ala Ile Leu
 85 90 95

Lys Arg Gln Leu His Asn Leu Gln Glu Asn His Arg Gln Met Met Gly
 100 105 110

Glu Glu Leu Ser Gly Leu Ser Val Glu Ala Leu Gln Asn Leu Glu Asn
 115 120 125

Gln Leu Glu Leu Ser Leu Arg Gly Val Arg Met Lys Lys Asp Gln Met
 130 135 140

Leu Ile Glu Glu Ile Gln Val Leu Asn Arg Glu Gly Asn Leu Val His
 145 150 155 160

Gln Glu Asn Leu Asp Leu His Lys Lys Val Asn Leu Met His Gln Gln
 165 170 175

Asn Met Glu Leu His Glu Lys Val Ser Glu Val Glu Gly Val Lys Ile
 180 185 190

Ala Asn Lys Asn Ser Leu Leu Thr Asn Gly Leu Asp Met Arg Asp Thr
 195 200 205

Ser Asn Glu His Val His Leu Gln Leu Ser Gln Pro Gln His Asp His
 210 215 220

Glu Thr His Ser Lys Ala Ile Gln Leu Asn Tyr Phe Ser Phe Ile Ala
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<210> 71

<211> 1552

<212> DNA

<213> Arabidopsis thaliana

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	gttctcgaaa	gatccattaa	aatcaaaacc	taagctctct	ctcttgcttc	taggggtttt	180		
	ttgttcgttg	tg atg	gcg aga	gaa aag	att cag	atc agg	aag atc	gac aac	231
		Met Ala	Arg Glu	Lys Ile	Gln Ile	Arg Lys	Ile Asp	Asn	
		1		5		10			
	gca acg	gcg aga	caa gtg	acg ttt	tcg aaa	cga aga	aga ggg	ctt ttc	279
	Ala Thr	Ala Arg	Gln Val	Thr Phe	Ser Lys	Arg Arg	Arg Gly	Leu Phe	
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	aag aaa	gct gaa	gaa ctc	tcc gtt	ctc tgc	gac gcc	gat gtc	gct ctc	327
	Lys Lys	Ala Glu	Glu Leu	Ser Ser	Val Leu	Cys Asp	Ala Asp	Val Ala	Leu
	30		35			40		45	
	atc atc	ttc tct	tcc acc	gga aaa	ctg ttc	gag ttc	tgt agc	tcc agc	375
	Ile Ile	Phe Ser	Ser Thr	Gly Lys	Leu Phe	Glu Phe	Cys Ser	Ser Ser	
			50		55		60		
	atg aag	gaa gtc	cta gag	agg cat	aac ttg	cag tca	aag aac	ttg gag	423
	Met Lys	Glu Val	Leu Glu	Arg His	Asn Leu	Gln Ser	Lys Asn	Leu Glu	
		65			70		75		
	aag ctt	gat cag	cca tct	ctt gag	tta cag	ctg gtt	gag aac	agt gat	471
	Lys Leu	Asp Gln	Pro Ser	Leu Glu	Leu Gln	Leu Val	Glu Asn	Ser Asp	
		80		85		90			
	cac gcc	cga atg	agt aaa	gaa att	gcg gac	aag agc	cac cga	cta agg	519
	His Ala	Arg Met	Ser Lys	Glu Ile	Ala Asp	Lys Ser	His Arg	Leu Arg	
	95			100		105			
	Gaa atg	aga gga	gag gaa	ctt caa	gga ctt	gac att	gaa gag	ctt cag	567
	Gln Met	Arg Gly	Glu Glu	Gln Glu	Lys Leu	Asp Ile	Glu Glu	Leu Gln	
	110		115			120		125	
	cag cta	gag aag	gcc ctt	gaa act	ggt ttg	acg cgt	gtg att	gaa aca	615
	Gln Leu	Glu Lys	Ala Leu	Glu Thr	Gly Leu	Thr Arg	Val Ile	Glu Thr	
			130		135		140		
	aag agt	gac aag	att atg	agt gag	atc agc	gaa ctt	cag aaa	aag gga	663
	Lys Ser	Asp Lys	Lys Ile	Met Ser	Glu Ile	Ser Glu	Leu Lys	Lys Gly	
		145			150		155		
	atg caa	ttg atg	gat gag	aac aag	cgg ttg	agg cag	caa gta	tgt gtc	711
	Met Gln	Leu Met	Asp Glu	Asn Lys	Arg Leu	Arg Gln	Gln Val	Cys Val	
	160			165		170			

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tta ccc tct ctg ttg ata aca aat ccc ttt ctt ttg tct acc att aac 759
Leu Pro Ser Leu Leu Ile Thr Asn Pro Phe Leu Leu Ser Thr Ile Asn
175 180 185

gta cac act cct aaa ttt aat ccc cag ttg tct aca aca cat atg ttt 807
Val His Thr Pro Lys Phe Asn Pro Gln Leu Ser Thr Thr His Met Phe
190 195 200 205

gat cat act gtg aga taaatgaata aaccaagtga tatagcgcgga tttaaaaaatg 862
Asp His Thr Val Arg
210

tcttttaaaac taaaggtaac catgtagcta gttagtctct aggggtcctag aggtctacga 922

gtgtgcatgc atggatttgg tgcgtttttt ctttttcac ttcattttgt tttttgaaac 982

aaggaaccat aaacgaatat atatctaatt cttgtttgat atatagtttg gtcgaggcct 1042

catgtcaaga tttgctcatt cgtagttagt tgatctctag agaaaattcaa aacacatggt 1102

gccactaaaa acacaaaaatg caaataactta gctagagaac ttaatgatat gttttgtctt 1162

gattttttgca gggaaacgcaa ctaacggaag agaacgagcg acttggcctg caaatatgta 1222

acaatgtgca tgcacacggt ggtgctgaat cggagaacgc tgctgtgtac gaggaaggac 1282

agtgcgcgga gtctattact aacgcgcgaa actctaccgg agcgctgtgt gactccgaga 1342

gtcccgacac ttcccttagg ctgcgcttac cgtatggtgg ttatagatgg aacaattcaa 1402

agaagttgat ggagtggagga gagtaatgta aatcttttta actcggttagt aacaagagac 1462

aatgtctaag tagtgaattc tcaaatgttt gtgtaagttt ctgcctatgg aagagcgttt 1522

cattttttatg attaaaaaaa aaaaaaaaaa 1552

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<213> Arabidopsis thaliana

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Arg Gln Val Thr Phe Ser Lys Arg Arg Arg Gly Leu Phe Lys Lys Ala
20 25 30

Glu Glu Leu Ser Val Leu Cys Asp Ala Asp Val Ala Leu Ile Ile Phe
35 40 45

Ser Ser Thr Gly Lys Leu Phe Glu Phe Cys Ser Ser Ser Met Lys Glu
50 55 60

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Val Leu Glu Arg His Asn Leu Gln Ser Lys Asn Leu Glu Lys Leu Asp
 65 70 75 80
 Gln Pro Ser Leu Glu Leu Gln Leu Val Glu Asn Ser Asp His Ala Arg
 85 90 95
 Met Ser Lys Glu Ile Ala Asp Lys Ser His Arg Leu Arg Gln Met Arg
 100 105 110
 Gly Glu Glu Leu Gln Gly Leu Asp Ile Glu Glu Leu Gln Gln Leu Glu
 115 120 125
 Lys Ala Leu Glu Thr Gly Leu Thr Arg Val Ile Glu Thr Lys Ser Asp
 130 135 140
 Lys Ile Met Ser Glu Ile Ser Glu Leu Gln Lys Lys Gly Met Gln Leu
 145 150 155 160
 Met Asp Glu Asn Lys Arg Leu Arg Gln Gln Val Cys Val Leu Pro Ser
 165 170 175
 Leu Leu Ile Thr Asn Pro Phe Leu Leu Ser Thr Ile Asn Val His Thr
 180 185 190
 Pro Lys Phe Asn Pro Gln Leu Ser Thr Thr His Met Phe Asp His Thr
 195 200 205
 Val Arg
 210
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 <222> (56)..(1018)
 <223> G866
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 Thr Val Asp Ile Met Arg Leu Pro Lys Met Glu Asp Gln Thr Ala Ile
 5 10 15
 caa gaa gct gca tca caa ggc tta aaa agc atg gaa cac ttg att cgt 154
 Gln Glu Ala Ala Ser Gln Gly Leu Lys Ser Met Glu His Leu Ile Arg
 20 25 30
 gtc ctc tct aac cgt ccc gaa gaa cgt aac gtt gat tgc tct gag atc 202
 Val Leu Ser Asn Arg Pro Glu Glu Arg Asn Val Asp Cys Ser Glu Ile
 35 40 45

tgt cca gcg agg aaa cac gtg gaa aga gct ttg gat gat tca acg atg 922
 Cys Pro Ala Arg Lys His Val Glu Arg Ala Leu Asp Asp Ser Thr Met
 275 280 285

ttg att gtg acg tac gaa gga gag cac cgt cat cac cag tcc acg atg 970
 Leu Ile Val Thr Tyr Glu Gly Glu His Arg His His Gln Ser Thr Met
 290 295 300 305

cag gag cat gta act cct agc gtg agt ggt ttg gtg ttt ggt tcg gct 1018
 Gln Glu His Val Thr Pro Ser Val Ser Gly Leu Val Phe Gly Ser Ala
 310 315 320

tgaagaatta attagtttgg tagttttggta atatttttgag aaatagagggg gttgggtttg 1078

taattttttt tctataacaa aattagtttt agattttttt ttagtagtct ttggaatgga 1138

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<212> PRT

<213> Arabidopsis thaliana

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<223> G866

<400> 74

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 20 25 30

Arg Val Leu Ser Asn Arg Pro Glu Glu Arg Asn Val Asp Cys Ser Glu
 35 40 45

Ile Thr Asp Phe Thr Val Ser Lys Phe Lys Lys Val Ile Ser Leu Leu
 50 55 60

Asn Arg Ser Gly His Ala Arg Phe Arg Arg Gly Pro Val His Ser Pro
 65 70 75 80

Pro Ser Ser Ser Val Pro Pro Pro Val Lys Val Thr Thr Pro Ala Pro
 85 90 95

Thr Gln Ile Ser Ala Pro Ala Pro Val Ser Phe Val Gln Ala Asn Gln
 100 105 110

Gln Ser Val Thr Leu Asp Phe Thr Arg Pro Ser Val Phe Gly Ala Lys
 115 120 125

Thr Lys Ser Ser Glu Val Val Glu Phe Ala Lys Glu Ser Phe Ser Val
 130 135 140

Ser Ser Asn Ser Ser Phe Met Ser Ser Ala Ile Thr Gly Asp Gly Ser
 145 150 155 160

Val Ser Lys Gly Ser Ser Ile Phe Leu Ala Pro Ala Pro Ala Val Pro
165 170 175

Val Thr Ser Ser Gly Lys Pro Pro Leu Ser Gly Leu Pro Tyr Arg Lys
180 185 190

Arg Cys Phe Glu His Asp His Ser Glu Gly Phe Ser Gly Lys Ile Ser
195 200 205

Gly Ser Gly Asn Gly Lys Cys His Cys Lys Lys Ser Arg Lys Asn Arg
210 215 220

Met Lys Arg Thr Val Arg Val Pro Ala Val Ser Ala Lys Ile Ala Asp
225 230 235 240

Ile Pro Pro Asp Glu Tyr Ser Trp Arg Lys Tyr Gly Gln Lys Pro Ile
245 250 255

Lys Gly Ser Pro His Pro Arg Gly Tyr Tyr Lys Cys Ser Thr Phe Arg
260 265 270

Gly Cys Pro Ala Arg Lys His Val Glu Arg Ala Leu Asp Asp Ser Thr
275 280 285

Met Leu Ile Val Thr Tyr Glu Gly Glu His Arg His His Gln Ser Thr
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Met Gln Glu His Val Thr Pro Ser Val Ser Gly Leu Val Phe Gly Ser
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<210> 75

<211> 2603

<212> DNA

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<220>

<221> CDS

<222> (397)..(2457)

<223> G877

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agagaggaag aaggagaaga aaaaaatatt tctttctctc cggtttcaa caaaatctct 180
cttttttctt tcatcagtgt taaattcggg tccgggtcgg gtgggttttc ggtttttggt 240
gttcggtatc gagcacagt ggatgttagc gacggaactg aggttttcag tttcggtcgt 300
cggcggtgtg gacggtgttt gtgtgtcgtc ttcttttatt aatcaggagt ttcacacag 360

[illegible]

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gac Asp	aat Asn	caa Gln	aac Asn	ggg Gly 235	cag Gln	aac Asn	aag Lys	aca Thr	tct Ser 240	gat Asp	gtc Val	act Thr	aca Thr	aac Asn 245	acc Thr	1134
agt Ser	ctt Leu	gaa Glu 250	acc Thr	gtg Val	gat Asp	cat His	caa Gln	gag Glu 255	gaa Glu	gaa Glu	gag Glu	caa Gln 260	aga Arg	cgc Arg		1182
ggt Gly	gat Asp	tcg Ser 265	atg Met	gct Ala	ggt Gly	ggt Gly	cgc Ala 270	cct Pro	gca Ala	gag Glu	gat Asp	gga Gly 275	tat Tyr	aac Asn	tgg Trp	1230
agg Arg 280	aaa Tyr	tac Gly	gga Gln	caa Gln	aag Lys	ttg Leu 285	gtc Val	aaa Lys	gga Gly	agt Ser	gag Glu 290	tat Tyr	ccg Pro	cga Arg	agc Ser	1278
tat Tyr 295	tac Tyr	aag Lys	gtc Cys	aca Thr	aac Asn 300	ccg Pro	aat Asn	tgt Cys	cag Gln	gtg Val 305	aag Lys	aag Lys	aaa Lys	gtt Val 310	gag Glu	1326
aga Arg	tca Ser	agg Arg	gaa Glu	ggt Gly 315	cac His	atc Ile	aca Thr	gag Glu	att Ile 320	ata Ile	tac Tyr	aaa Lys	gga Gly	gct Ala 325	cat His	1374
aat Asn	cat His	ctt Leu	aaa Lys 330	cct Pro	cca Pro	cct Pro	aat Asn	cgc Arg 335	cgc Arg	tca Arg	ggg Gly	atg Met		gta Val 340	gat Asp	1422
gga Gly	act Thr	gaa Glu	caa Gln	gtt Val	gaa Glu	caa Gln	caa Gln	caa Gln	caa Gln	cag Gln	aga Arg	gat Asp 355	tct Ser	gct Ala	gca Ala	1470
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gtg Val	gtt Val	gtg Val	gtt Val	gat Asp	gct Ala	tct Ser	tca Ser	aca Thr	ttc Phe 415	tct Ser	aat Asn	gat Asp	gaa Glu 420	gat Asp	gaa Glu	1662
gat Asp	gat Asp	cga Arg 425	ggg Gly	aca Thr	cat His	gga Gly	agt Ser 430	gtt Val	tct Ser	ttg Leu	ggt Gly	tac Tyr 435	gat Asp	gga Gly	gga Gly	1710

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ggg tta gcg tat ggt caa ggg aaa atg ccg ggt ttg cct cac ccg tat Gly Leu Ala Tyr Gly Gln Gly Lys Met Pro Gly Leu Pro His Pro Tyr 635 640 645	2334
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00304510:001300

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 665 670 675

cag atc atg agt aga tta cct cag att tgaaatttac tcttcttctt 2477
 Gln Ile Met Ser Arg Leu Pro Gln Ile
 680 685

cttctctctgc atttggtcac tccttataat aacttttaat ttctgcttct tcttcttctt 2537

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aaaaaa 2603

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<211> 687

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G877

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 20 25 30

Lys Ser Ser Lys Arg Val Leu Glu Arg Glu Leu Ser Leu Asn His Gly
 35 40 45

Gln Val Ile Gly Leu Glu Glu Asp Thr Ser Ser Asn His Asn Lys Asp
 50 55 60

Ser Ser Gln Ser Asn Val Phe Arg Gly Gly Leu Ser Glu Arg Ile Ala
 65 70 75 80

Ala Arg Ala Gly Phe Asn Ala Pro Arg Leu Asn Thr Glu Asn Ile Arg
 85 90 95

Thr Asn Thr Asp Phe Ser Ile Asp Ser Asn Leu Arg Ser Pro Cys Leu
 100 105 110

Thr Ile Ser Ser Pro Gly Leu Ser Pro Ala Thr Leu Leu Glu Ser Pro
 115 120 125

Val Phe Leu Ser Asn Pro Leu Ala Gln Pro Ser Pro Thr Thr Gly Lys
 130 135 140

Phe Pro Phe Leu Pro Gly Val Asn Gly Asn Ala Leu Ser Ser Glu Lys
 145 150 155 160

Ala Lys Asp Glu Phe Phe Asp Asp Ile Gly Ala Ser Phe Ser Phe His
 165 170 175


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Ser Asp Val Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly
          485                      490                      495

Gln Lys Val Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys
          500                      505                      510

Thr Ala Pro Gly Cys Thr Val Arg Lys His Val Glu Arg Ala Ser His
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Asp Leu Lys Ser Val Ile Thr Thr Tyr Glu Gly Lys His Asn His Asp
          530                      535                      540

Val Pro Ala Ala Arg Asn Ser Ser His Gly Gly Gly Gly Asp Ser Gly
          545                      550                      555                      560

Asn Gly Asn Ser Gly Gly Ser Ala Ala Val Ser His His Tyr His Asn
          565                      570                      575

Gly His His Ser Glu Pro Pro Arg Gly Arg Phe Asp Arg Gln Val Thr
          580                      585                      590

Thr Asn Asn Gln Ser Pro Phe Ser Arg Pro Phe Ser Phe Gln Pro His
          595                      600                      605

Leu Gly Pro Pro Ser Gly Phe Ser Phe Gly Leu Gly Gln Thr Gly Leu
          610                      615                      620

Val Asn Leu Ser Met Pro Gly Leu Ala Tyr Gly Gln Gly Lys Met Pro
          625                      630                      635                      640

Gly Leu Pro His Pro Tyr Met Thr Gln Pro Val Gly Met Ser Glu Ala
          645                      650                      655

Met Met Gln Arg Gly Met Glu Pro Lys Val Glu Pro Val Ser Asp Ser
          660                      665                      670

Gly Gln Ser Val Tyr Asn Gln Ile Met Ser Arg Leu Pro Gln Ile
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<223> G878

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may be A, T, C, G, other or unknown

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tcaaaatcaa gaatcg atg gcg gag aag gaa gaa aaa gaa cca tgc aag tta 232

Met Ala Glu Lys Glu Glu Lys Glu Pro Ser Lys Leu

1

5

10

aaa tca tcc acc gga gtt tca cgg cca acg att tca cta cct cct cga 280

Lys Ser Ser Thr Gly Val Ser Arg Pro Thr Ile Ser Leu Pro Pro Arg

15

20

25

ccg ttt ggt gaa atg ttt ttt agc ggt ggc gtt gga ttt agt cct gga 328

Pro Phe Gly Glu Met Phe Phe Ser Ser Gly Gly Val Gly Phe Ser Pro Gly

30

35

40

cca atg act ctc gtc tca aat tta ttc tct gat cct gat gag ttc aag 376

Pro Met Thr Leu Val Ser Asn Leu Phe Ser Asp Pro Asp Glu Phe Lys

45

50

55

60

tct ttc tct cag ctt tta gct gga gct atg gct tct cct ccg ccg gca gct 424

Ser Phe Ser Ser Gln Leu Leu Ala Gly Ala Met Ala Ser Pro Ala Ala Ala

65

70

75

gct gtt gcc gcc gct gct gtg gtt gct act gct cat cat cag aca cct 472

Ala Val Ala Ala Ala Val Val Ala Thr Ala His His Gln Thr Pro

80

85

90

gtg agc tct gtc ggt gat ggc ggt gga agc ggt ggt gat gtt gac ccg 520

Val Ser Ser Val Gly Asp Gly Gly Gly Ser Gly Gly Asp Val Asp Pro

95

100

105

agg ttt aag cag agt aga cca acg gga ttg atg ata act caa cca ccg 568

Arg Phe Lys Gln Ser Arg Pro Thr Gly Leu Met Ile Thr Gln Pro Pro

110

115

120

ggg atg ttt act gta ccg ccg ggg tta agt ccg gct act ctt ttg gat 616

Gly Met Phe Thr Val Pro Pro Gly Leu Ser Pro Ala Thr Leu Leu Asp

125

130

135

140

tct ccg agc ttc ttt ggt ctt ttt tca cct ctt cag gga aca ttt ggt 664

Ser Pro Ser Phe Phe Gly Leu Phe Ser Pro Leu Gln Gly Thr Phe Gly

145

150

155

atg aca cat caa caa gct tta gca caa gtc act gca caa gca gtt caa 712

Met Thr His Gln Gln Ala Leu Ala Gln Val Thr Ala Gln Ala Val Gln

160

165

170

ggc aat aat gtt cat atg cag caa tca caa caa tct gaa tat cct tct 760

Gly Asn Asn Val His Met Gln Gln Ser Gln Gln Ser Glu Tyr Pro Ser

175

180

185

tct aca caa caa caa caa caa caa caa caa gct tca ttg act gag 808

Ser Thr Gln Gln Gln Gln Gln Gln Gln Gln Ala Ser Leu Thr Glu

190

195

200

att cca tca ttt tct tct gca cct agg tct cag att cga gcc tcg gtt 856

Ile Pro Ser Phe Ser Ser Ala Pro Arg Ser Ile Arg Ala Ser Val

205

210

215

220

caa gaa aca tgc	cag ggt	cag aga	gag act	tgc gaa	ata tct	gtc ttt	904
Gln Glu Thr Ser	Gln Gly	Gln Arg	Glu Thr	Ser Glu	Ile Ser	Val Phe	
	225		230		235		
gag cat cgg tca	cag cct	caa aat	gct gac	aaa cca	gct gat	gat gga	952
Glu His Arg Ser	Gln Pro	Gln Asn	Ala Asp	Lys Pro	Ala Asp	Asp Gly	
	240		245		250		
tac aac tgg cgg	aaa tat	ggg cag	aag caa	gtg aag	ggg agc	gat ttt	1000
Tyr Asn Trp Arg	Lys Tyr	Gly Gln	Lys Gln	Val Lys	Gly Ser	Asp Phe	
	255		260		265		
cct cgg agt tat	tac aaa	tgt acg	cat cca	gct tgt	cct gtc	aag aag	1048
Pro Arg Ser Tyr	Tyr Lys	Cys Thr	His Pro	Ala Cys	Pro Val	Lys Lys	
	270		275		280		
aaa gtg gag agg	tca ctc	gat gga	caa gta	acg gaa	atc atc	tac aag	1096
Lys Val Glu Arg	Ser Leu	Asp Gly	Gln Val	Thr Glu	Ile Ile	Tyr Lys	
	285		290		295	300	
ggg caa cac aat	cat gag	ctt cct	caa aag	cgc ggt	aac aat	aac ggg	1144
Gly Gln His Asn	His Glu	Leu Pro	Gln Lys	Arg Gly	Asn Asn	Asn Gly	
	305		310		315		
agt tgt aaa agt	tct gat	att gca	aat cag	ttt caa	aca agt	aat agc	1192
Ser Cys Lys Ser	Ser Asp	Ile Ala	Asn Gln	Phe Gln	Thr Ser	Asn Ser	
	320		325		330		
agt ctc aac aag	agt aag	agg gac	cag gaa	aca agc	caa gtt	aca aca	1240
Ser Leu Asn Lys	Ser Lys	Arg Asp	Gln Glu	Thr Ser	Gln Val	Thr Thr	
	335		340		345		
aca gag cag atg	tct gaa	gca agt	gat agc	gag gag	gtt ggg	aat gca	1288
Thr Glu Gln Met	Ser Glu	Ala Ser	Asp Ser	Glu Glu	Val Gly	Asn Ala	
	350		355		360		
gag act agt gtg	gga gaa	aga cat	gag gat	gag cct	gat ccc	aag cga	1336
Glu Thr Ser Val	Gly Glu	Arg His	Glu Asp	Glu Pro	Asp Pro	Lys Arg	
	365		370		375	380	
aga aat aca gaa	gtt cgg	gtt tca	gaa cca	gtt gct	tca tgc	cat aga	1384
Arg Asn Thr Glu	Val Arg	Val Ser	Glu Pro	Val Ala	Ser Ser	His Arg	
	385		390		395		
act gtg aca gag	cct agg	att att	gtc caa	acg acg	agt gaa	gtt gac	1432
Thr Val Thr Glu	Pro Arg	Ile Ile	Val Gln	Thr Thr	Ser Glu	Val Asp	
	400		405		410		
ctc tta gat gat	gga tat	agg tgg	cgc aag	tat ggt	cag aaa	gta gtc	1480
Leu Leu Asp Asp	Gly Tyr	Arg Trp	Arg Lys	Tyr Gly	Gln Lys	Val Val	
	415		420		425		
aaa gga aat cct	tat ccg	agg agc	tac tat	aag tgt	aca aca	cca gat	1528
Lys Gly Asn Pro	Tyr Pro	Arg Ser	Tyr Tyr	Lys Cys	Thr Thr	Pro Asp	
	430		435		440		

Ala Ala Val Val Ala Thr Ala His His Gln Thr Pro Val Ser Ser Val
85 90 95

Gly Asp Gly Gly Gly Ser Gly Gly Asp Val Asp Pro Arg Phe Lys Gln
 100 105 110
 Ser Arg Pro Thr Gly Leu Met Ile Thr Gln Pro Pro Gly Met Phe Thr
 115 120 125
 Val Pro Pro Gly Leu Ser Pro Ala Thr Leu Leu Asp Ser Pro Ser Phe
 130 135 140
 Phe Gly Leu Phe Ser Pro Leu Gln Gly Thr Phe Gly Met Thr His Gln
 145 150 155 160
 Gln Ala Leu Ala Gln Val Thr Ala Gln Ala Val Gln Gly Asn Asn Val
 165 170 175
 His Met Gln Gln Ser Gln Gln Ser Glu Tyr Pro Ser Ser Thr Gln Gln
 180 185 190
 Gln Gln Gln Gln Gln Gln Gln Ala Ser Leu Thr Glu Ile Pro Ser Phe
 195 200 205
 Ser Ser Ala Pro Arg Ser Gln Ile Arg Ala Ser Val Gln Glu Thr Ser
 210 215 220
 Gln Gly Gln Arg Glu Thr Ser Glu Ile Ser Val Phe Glu His Arg Ser
 225 230 235 240
 Gln Pro Gln Asn Ala Asp Lys Pro Ala Asp Asp Gly Tyr Asn Trp Arg
 245 250 255
 Lys Tyr Gly Gln Lys Gln Val Lys Gly Ser Asp Phe Pro Arg Ser Tyr
 260 265 270
 Tyr Lys Cys Thr His Pro Ala Cys Pro Val Lys Lys Lys Val Glu Arg
 275 280 285
 Ser Leu Asp Gly Gln Val Thr Glu Ile Ile Tyr Lys Gly Gln His Asn
 290 295 300
 His Glu Leu Pro Gln Lys Arg Gly Asn Asn Asn Gly Ser Cys Lys Ser
 305 310 315 320
 Ser Asp Ile Ala Asn Gln Phe Gln Thr Ser Asn Ser Ser Leu Asn Lys
 325 330 335
 Ser Lys Arg Asp Gln Glu Thr Ser Gln Val Thr Thr Thr Glu Gln Met
 340 345 350
 Ser Glu Ala Ser Asp Ser Glu Glu Val Gly Asn Ala Glu Thr Ser Val
 355 360 365
 Gly Glu Arg His Glu Asp Glu Pro Asp Pro Lys Arg Arg Asn Thr Glu
 370 375 380
 Val Arg Val Ser Glu Pro Val Ala Ser Ser His Arg Thr Val Thr Glu
 385 390 395 400

Pro Arg Ile Ile Val Gln Thr Thr Ser Glu Val Asp Leu Leu Asp Asp
405 410 415

Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Val Val Lys Gly Asn Pro
420 425 430

Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr Thr Pro Asp Cys Gly Val Arg
435 440 445

Lys His Val Glu Arg Ala Ala Thr Asp Pro Lys Ala Val Val Thr Thr
450 455 460

Tyr Glu Gly Lys His Asn His Asp Val Pro Ala Ala Arg Thr Ser Ser
465 470 475 480

His Gln Leu Arg Pro Asn Asn Gln His Asn Thr Ser Thr Val Asn Phe
485 490 495

Asn His Gln Gln Pro Val Ala Arg Leu Arg Leu Lys Glu Glu Gln Ile
500 505 510

Thr

<210> 79
<211> 1207
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (67)..(1050)
<223> G883

<400> 79
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atcatc atg gcc gtc gat cta atg cgt ttc cct aag ata gat gat caa 108
Met Ala Val Asp Leu Met Arg Phe Pro Lys Ile Asp Asp Gln
1 5 10

acg gct att cag gaa gct gca tcg caa ggt tta caa agt atg gaa cat 156
Thr Ala Ile Gln Glu Ala Ala Ser Gln Gly Leu Gln Ser Met Glu His
15 20 25 30

ctg atc cgt gtc ctc tct aac cgt ccc gaa caa caa cac aac gtt gac 204
Leu Ile Arg Val Leu Ser Asn Arg Pro Glu Gln Gln His Asn Val Asp
35 40 45

tgc tcc gag atc act gac ttc acc gtt tct aaa ttc aaa acc gtc att 252
Cys Ser Glu Ile Thr Asp Phe Thr Val Ser Lys Phe Lys Thr Val Ile
50 55 60

tct ctc ctt aac cgt act ggt cac gct cgg ttc aga cgc gga ccg gtt 300
Ser Leu Leu Asn Arg Thr Gly His Ala Arg Phe Arg Arg Gly Pro Val
65 70 75

cac tcc act tcc tct gcc gca tct cag aaa cta cag agt cag atc gtt	348
His Ser Thr Ser Ser Ala Ala Ser Gln Lys Leu Gln Ser Gln Ile Val	
80 85 90	
aaa aat act caa cct gag gct ccg att gtt tct cag cca gtg aga aca	396
Lys Asn Thr Gln Pro Glu Ala Pro Ile Val Ser Gln Pro Val Arg Thr	
95 100 105 110	
act acg aat cac cct caa atc gtt cct cca ccg tct agt gta aca ctc	444
Thr Thr Asn His Pro Gln Ile Val Pro Pro Ser Ser Val Thr Leu	
115 120 125	
gat ttc tct aaa cca agc atc ttc ggc acc aaa gct aag agc gcc gag	492
Asp Phe Ser Lys Pro Ser Ile Phe Gly Thr Lys Ala Lys Ser Ala Glu	
130 135 140	
ctg gaa ttc tcc aaa gaa aac ttc agt gtt tct tta aac tcc tca ttc	540
Leu Glu Phe Ser Lys Glu Asn Phe Ser Val Ser Leu Asn Ser Ser Phe	
145 150 155	
atg tcg tcg gcg ata acc gga gac ggc agc gtc tcc aat gga aaa atc	588
Met Ser Ser Ala Ile Thr Gly Asp Gly Ser Val Ser Asn Gly Lys Ile	
160 165 170	
ttc ctt gct tct gct ccg tcg cag cct gtt aac tct tcc gga aaa cca	636
Phe Leu Ala Ser Ala Pro Ser Gln Pro Val Asn Ser Ser Gly Lys Pro	
175 180 185 190	
ccg ttg gct ggt cat cct tac aga aag aga tgt ctc gag cat gag cac	684
Pro Leu Ala Gly His Pro Tyr Arg Lys Arg Cys Leu Glu His Glu His	
195 200 205	
tca gag agt ttc tcc gga aaa gtc tcc ggc tcc gcc tac gga aag tgc	732
Ser Glu Ser Phe Ser Gly Lys Val Ser Gly Ser Ala Tyr Gly Lys Cys	
210 215 220	
cat tgc aag aaa agg aaa aat cgg atg aag aga acc gtg aga gta ccg	780
His Cys Lys Lys Arg Lys Asn Arg Met Lys Arg Thr Val Arg Val Pro	
225 230 235	
gcg ata agt gca aag atc gcc gat att cca ccg gac gaa tat tcg tgg	828
Ala Ile Ser Ala Lys Ile Ala Asp Ile Pro Pro Asp Glu Tyr Ser Trp	
240 245 250	
agg aag tac gga caa aaa ccg atc aag ggc tca cca cac cca cgt ggt	876
Arg Lys Tyr Gly Gln Lys Pro Ile Lys Gly Ser Pro His Pro Arg Gly	
255 260 265 270	
tac tac aag tgc agt aca ttc aga gga tgt cca gcg agg aaa cac gtg	924
Tyr Tyr Lys Cys Ser Thr Phe Arg Gly Cys Pro Ala Arg Lys His Val	
275 280 285	
gaa cga gca tta gat gat cca gcg atg ctt att gtg aca tac gaa gga	972
Glu Arg Ala Leu Asp Asp Pro Ala Met Leu Ile Val Thr Tyr Glu Gly	
290 295 300	

gag cac cgt cat aac caa tcc gcg atg cag gag aat att tct tct tca 1020
 Glu His Arg His Asn Gln Ser Ala Met Gln Glu Asn Ile Ser Ser Ser
 305 310 315

ggc att aat gat tta gtg ttt gcc tcg gct tgactttttt ttgtactatt 1070
 Gly Ile Asn Asp Leu Val Phe Ala Ser Ala
 320 325

tggttttttga ttttttgagt acttttagatg gattgaaatt tgtaaatttt tttattaaga 1130

aatcaatttta aatagagaaa aattagtggg ggtgcaaaaa aaaaaaaaaa aaaaaaaaaa 1190

aaaaaaaaaa aaaaaaaa 1207

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<211> 328

<212> PRT

<213> *Arabidopsis thaliana*

<220>

<223> G883

<400> 80

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Ile Gln Glu Ala Ala Ser Gln Gly Leu Gln Ser Met Glu His Leu Ile
 20 25 30

Arg Val Leu Ser Asn Arg Pro Glu Gln Gln His Asn Val Asp Cys Ser
 35 40 45

Glu Ile Thr Asp Phe Thr Val Ser Lys Phe Lys Thr Val Ile Ser Leu
 50 55 60

Leu Asn Arg Thr Gly His Ala Arg Phe Arg Arg Gly Pro Val His Ser
 65 70 75 80

Thr Ser Ser Ala Ala Ser Gln Lys Leu Gln Ser Gln Ile Val Lys Asn
 85 90 95

Thr Gln Pro Glu Ala Pro Ile Val Ser Gln Pro Val Arg Thr Thr Thr
 100 105 110

Asn His Pro Gln Ile Val Pro Pro Pro Ser Ser Val Thr Leu Asp Phe
 115 120 125

Ser Lys Pro Ser Ile Phe Gly Thr Lys Ala Lys Ser Ala Glu Leu Glu
 130 135 140

Phe Ser Lys Glu Asn Phe Ser Val Ser Leu Asn Ser Ser Phe Met Ser
 145 150 155 160

Ser Ala Ile Thr Gly Asp Gly Ser Val Ser Asn Gly Lys Ile Phe Leu
 165 170 175

Ala Ser Ala Pro Ser Gln Pro Val Asn Ser Ser Gly Lys Pro Pro Leu
180 185 190

Ala Gly His Pro Tyr Arg Lys Arg Cys Leu Glu His Glu His Ser Glu
195 200 205

Ser Phe Ser Gly Lys Val Ser Gly Ser Ala Tyr Gly Lys Cys His Cys
210 215 220

Lys Lys Arg Lys Asn Arg Met Lys Arg Thr Val Arg Val Pro Ala Ile
225 230 235 240

Ser Ala Lys Ile Ala Asp Ile Pro Pro Asp Glu Tyr Ser Trp Arg Lys
245 250 255

Tyr Gly Gln Lys Pro Ile Lys Gly Ser Pro His Pro Arg Gly Tyr Tyr
260 265 270

Lys Cys Ser Thr Phe Arg Gly Cys Pro Ala Arg Lys His Val Glu Arg
275 280 285

Ala Leu Asp Asp Pro Ala Met Leu Ile Val Thr Tyr Glu Gly Glu His
290 295 300

Arg His Asn Gln Ser Ala Met Gln Glu Asn Ile Ser Ser Ser Gly Ile
305 310 315 320

Asn Asp Leu Val Phe Ala Ser Ala
325

<210> 81

<211> 1879

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (31)..(1572)

<223> G884

<400> 81

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1 5

tcg aca tcg aag tcc acc gga gct ccg tcg cgt ccg act tta tct ctt 102
Ser Thr Ser Lys Ser Thr Gly Ala Pro Ser Arg Pro Thr Leu Ser Leu
10 15 20

cct cca cgg ccg ttt agt gag atg ttc ttt aac ggt ggc gtt gga ttc 150
Pro Pro Arg Pro Phe Ser Glu Met Phe Phe Asn Gly Gly Val Gly Phe
25 30 35 40

agt cct ggt ccg atg act ctg gtc tct aat atg ttc cct gat tcc gat 198
Ser Pro Gly Pro Met Thr Leu Val Ser Asn Met Phe Pro Asp Ser Asp
45 50 55

cgg cta agg ctt aaa gaa gag caa aca act tgagagaaga aaactcttga 1592
 Arg Leu Arg Leu Lys Glu Glu Gln Thr Thr
 505 510

ccgttttttca ttacaaaagc ttcaaaattc cactcacaca cttgtctgaa aaatctagca 1652
 gtttgcagga aagaacagc ttcaagaggt tgtagttctt ctatgttctg gtgtaaaact 1712
 taaaagcttt ttagggtttt cagatttctg ttactaata ctgtatgtga attcttttgt 1772
 acatgaggaa gaaaattaca gggggatatt ttgtgttgta tcttttgtgt tattgtttca 1832
 gtaaaagata ggtctttacat ttgtgtgtaaa aaaaaaaaaa aaaaaaa 1879

<210> 82
 <211> 514
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G884

<400> 82
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 20 25 30
 Phe Phe Asn Gly Gly Val Gly Phe Ser Pro Gly Pro Met Thr Leu Val
 35 40 45
 Ser Asn Met Phe Pro Asp Ser Asp Glu Phe Arg Ser Phe Ser Gln Leu
 50 55 60
 Leu Ala Gly Ala Met Ser Ser Pro Ala Thr Ala Ala Ala Ala Ala Ala
 65 70 75 80
 Ala Ala Thr Ala Ser Asp Tyr Gln Arg Leu Gly Glu Gly Thr Asn Ser
 85 90 95
 Ser Ser Gly Asp Val Asp Pro Arg Phe Lys Gln Asn Arg Pro Thr Gly
 100 105 110
 Leu Met Ile Ser Gln Ser Gln Ser Pro Ser Met Phe Thr Val Pro Pro
 115 120 125
 Gly Leu Ser Pro Ala Met Leu Leu Asp Ser Pro Ser Phe Leu Gly Leu
 130 135 140
 Phe Ser Pro Val Gln Gly Ser Tyr Gly Met Thr His Gln Gln Ala Leu
 145 150 155 160
 Ala Gln Val Thr Ala Gln Ala Val Gln Ala Asn Ala Asn Met Gln Pro
 165 170 175

Gln Thr Glu Tyr Pro Pro Pro Ser Gln Val Gln Ser Phe Ser Ser Gly
 180 185 190
 Gln Ala Gln Ile Pro Thr Ser Ala Pro Leu Pro Ala Gln Arg Glu Thr
 195 200 205
 Ser Asp Val Thr Ile Ile Glu His Arg Ser Gln Gln Pro Leu Asn Val
 210 215 220
 Asp Lys Pro Ala Asp Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys
 225 230 235 240
 Gln Val Lys Gly Ser Glu Phe Pro Arg Ser Tyr Tyr Lys Cys Thr Asn
 245 250 255
 Pro Gly Cys Pro Val Lys Lys Lys Val Glu Arg Ser Leu Asp Gly Gln
 260 265 270
 Val Thr Glu Ile Ile Tyr Lys Gly Gln His Asn His Glu Pro Pro Gln
 275 280 285
 Asn Thr Lys Arg Gly Asn Lys Asp Asn Thr Ala Asn Ile Asn Gly Ser
 290 295 300
 Ser Ile Asn Asn Asn Arg Gly Ser Ser Glu Leu Gly Ala Ser Gln Phe
 305 310 315 320
 Gln Thr Asn Ser Ser Asn Lys Thr Lys Arg Glu Gln His Glu Ala Val
 325 330 335
 Ser Gln Ala Thr Thr Thr Glu His Leu Ser Glu Ala Ser Asp Gly Glu
 340 345 350
 Glu Val Gly Asn Gly Glu Thr Asp Val Arg Glu Lys Asp Glu Asn Glu
 355 360 365
 Pro Asp Pro Lys Arg Arg Ser Thr Glu Val Arg Ile Ser Glu Pro Ala
 370 375 380
 Pro Ala Ala Ser His Arg Thr Val Thr Glu Pro Arg Ile Ile Val Gln
 385 390 395 400
 Thr Thr Ser Glu Val Asp Leu Leu Asp Asp Gly Tyr Arg Trp Arg Lys
 405 410 415
 Tyr Gly Gln Lys Val Val Lys Gly Asn Pro Tyr Pro Arg Ser Tyr Tyr
 420 425 430
 Lys Cys Thr Thr Pro Gly Cys Gly Val Arg Lys His Val Glu Arg Ala
 435 440 445
 Ala Thr Asp Pro Lys Ala Val Val Thr Thr Tyr Glu Gly Lys His Asn
 450 455 460
 His Asp Leu Pro Ala Ala Lys Ser Ser Ser His Ala Ala Ala Ala Ala
 465 470 475 480

180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480

Gln Leu Arg Pro Asp Asn Arg Pro Gly Gly Leu Ala Asn Leu Asn Gln
485 490 495

Gln Gln Gln Gln Gln Pro Val Ala Arg Leu Arg Leu Lys Glu Glu Gln
500 505 510

Thr Thr

<210> 83
<211> 1296
<212> DNA
<213> *Arabidopsis thaliana*

<220>
<221> CDS
<222> (114)..(1151)
<223> G920

<400> 83
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atactaaaaa cctaaaaaaa gttacatatt cattgtatct ttgtgagaaa aaa atg 116
Met
1
gat tcg aat agt aac aac acg aaa tcc ata aag aga aaa gtt gtc gac 164
Asp Ser Asn Ser Asn Asn Thr Lys Ser Ile Lys Arg Lys Val Val Asp
5 10 15
caa ctt gtc gaa ggc tat gaa ttc gct act cag ctt cag ctt ctc ctt 212
Gln Leu Val Glu Gly Tyr Glu Phe Ala Thr Gln Leu Gln Leu Leu Leu
20 25 30
tct cat caa cac tct aac cag tac cac atc gat gag acc cgt ctt gtt 260
Ser His Gln His Ser Asn Gln Tyr His Ile Asp Glu Thr Arg Leu Val
35 40 45
tcc ggg tcg ggt tca gtt tcc ggt ggt cca gat ccc gtt gat gag ctc 308
Ser Gly Ser Gly Ser Val Ser Gly Gly Pro Asp Pro Val Asp Glu Leu
50 55 60 65
atg tct aag atc ttg gga tct ttc cat aaa act ata tcg gtt ctt gat 356
Met Ser Lys Ile Leu Gly Ser Phe His Lys Thr Ile Ser Val Leu Asp
70 75 80
tct ttt gat ccc gtc gcc gtc tct gtc ccc atc gcc gtc gag ggt tca 404
Ser Phe Asp Pro Val Ala Val Ser Val Pro Ile Ala Val Glu Gly Ser
85 90 95
tgg aat gct tca tgt ggg gat gat tcg gcg act cgg gtg agt tgc aac 452
Trp Asn Ala Ser Cys Gly Asp Asp Ser Ala Thr Pro Val Ser Cys Asn
100 105 110
ggg gga gat tcc ggt gag agt aag aag aag aga tta ggg gtt ggt aag 500
Gly Gly Asp Ser Gly Glu Ser Lys Lys Lys Arg Leu Gly Val Gly Lys
115 120 125

tatgtttgat aaaaacacca tatatacttc tctttttaca ccaaaaaaaaaa aaaaaaaaaa 1291

aaaaa

1296

<210> 84

<211> 346

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G920

<400> 84

Met Asp Ser Asn Ser Asn Asn Thr Lys Ser Ile Lys Arg Lys Val Val
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Asp Gln Leu Val Glu Gly Tyr Glu Phe Ala Thr Gln Leu Gln Leu Leu
20 25 30

Leu Ser His Gln His Ser Asn Gln Tyr His Ile Asp Glu Thr Arg Leu
35 40 45

Val Ser Gly Ser Gly Ser Val Ser Gly Gly Pro Asp Pro Val Asp Glu
50 55 60

Leu Met Ser Lys Ile Leu Gly Ser Phe His Lys Thr Ile Ser Val Leu
65 70 75 80

Asp Ser Phe Asp Pro Val Ala Val Ser Val Pro Ile Ala Val Glu Gly
85 90 95

Ser Trp Asn Ala Ser Cys Gly Asp Asp Ser Ala Thr Pro Val Ser Cys
100 105 110

Asn Gly Gly Asp Ser Gly Glu Ser Lys Lys Lys Arg Leu Gly Val Gly
115 120 125

Lys Gly Lys Arg Gly Cys Tyr Thr Arg Lys Thr Arg Ser His Thr Arg
130 135 140

Ile Val Glu Ala Lys Ser Ser Glu Asp Arg Tyr Ala Trp Arg Lys Tyr
145 150 155 160

Gly Gln Lys Glu Ile Leu Asn Thr Thr Phe Pro Arg Ser Tyr Phe Arg
165 170 175

Cys Thr His Lys Pro Thr Gln Gly Cys Lys Ala Thr Lys Gln Val Gln
180 185 190

Lys Gln Asp Gln Asp Ser Glu Met Phe Gln Ile Thr Tyr Ile Gly Tyr
195 200 205

His Thr Cys Thr Ala Asn Asp Gln Thr His Ala Lys Thr Glu Pro Phe
210 215 220

Asp Gln Glu Ile Ile Met Asp Ser Glu Lys Thr Leu Ala Ala Ser Thr
225 230 235 240

Ala Gln Asn His Val Asn Ala Met Val Gln Glu Gln Glu Asn Asn Thr
245 250 255

Ser Ser Val Thr Ala Ile Asp Ala Gly Met Val Lys Glu Glu Gln Asn
260 265 270

Asn Asn Gly Asp Gln Ser Lys Asp Tyr Tyr Glu Gly Ser Ser Thr Gly
275 280 285

Glu Asp Leu Ser Leu Val Trp Gln Glu Thr Met Met Phe Asp Asp His
290 295 300

Gln Asn His Tyr Tyr Cys Gly Glu Thr Ser Thr Thr Ser His Gln Phe
305 310 315 320

Gly Phe Ile Asp Asn Asp Asp Gln Phe Ser Ser Phe Phe Asp Ser Tyr
325 330 335

Cys Ala Asp Tyr Glu Arg Thr Ser Ala Met
340 345

<210> 85

<211> 1130

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (116)..(1021)

<223> G921

<220>

<223> "n" at various positions throughout the sequence
may be A, T, C, G, other or unknown

<400> 85

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cacacatata catccacaag aacctcatatc gaagattcat cctacatata ttta atg 118
Met
1

gat cag tac tca tcc tct ttg gtc gat act tca tta gat ctc act att 166
Asp Gln Tyr Ser Ser Ser Leu Val Asp Thr Ser Leu Asp Leu Thr Ile
5 10 15

ggc gtt act cgt atg cga gtt gaa gaa gat cca ccg aca agt gct ttg 214
Gly Val Thr Arg Met Arg Val Glu Glu Asp Pro Pro Thr Ser Ala Leu
20 25 30

gtg gaa gaa tta aac cga gtt agt gct gag aac aag aag ctc tcg gag 262
Val Glu Glu Leu Asn Arg Val Ser Ala Glu Asn Lys Lys Leu Ser Glu
35 40 45

atg cta act ttg atg tgt gac aac tac aac gtc ttg agg aag caa ctt 310
 Met Leu Thr Leu Met Cys Asp Asn Tyr Asn Val Leu Arg Lys Gln Leu
 50 55 60 65

atg gaa tat gtt aac aag agc aac ata acc gag agg gat caa atc agc 358
 Met Glu Tyr Val Asn Lys Ser Asn Ile Thr Glu Arg Asp Gln Ile Ser
 70 75 80

cct ccc aag aaa cgc aaa tcc ccg gcg aga gag gac gca ttc agc tgc 406
 Pro Pro Lys Lys Arg Lys Ser Pro Ala Arg Glu Asp Ala Phe Ser Cys
 85 90 95

gcg gtt att ggc gga gtg tgg gag agt agc tca acg gat caa gat gag 454
 Ala Val Ile Gly Gly Val Ser Glu Ser Ser Ser Thr Asp Gln Asp Glu
 100 105 110

tat ttg tgt aag aag cag aga gaa gag act gtc gtg aag gag aaa gtc 502
 Tyr Leu Cys Lys Lys Gln Arg Glu Glu Thr Val Val Lys Glu Lys Val
 115 120 125

tca agg gtc tat tac aag acc gaa gct tct gac act acc ctc gtt gtg 550
 Ser Arg Val Tyr Tyr Lys Thr Glu Ala Ser Asp Thr Thr Leu Val Val
 130 135 140 145

aaa gat ggg tat caa tgg agg aaa tat gga cag aaa gtg act aga gac 598
 Lys Asp Gly Tyr Gln Trp Arg Lys Tyr Gly Gln Lys Val Thr Arg Asp
 150 155 160

aat cca tct cca aga gct tac ttc aaa tgt gct tgt gct cca agc tgt 646
 Asn Pro Ser Pro Arg Ala Tyr Phe Lys Cys Ala Cys Ala Pro Ser Cys
 165 170 175

tct gtc aaa aag aag gtt cag aga agt gtg gag gat cag tcc gtg tta 694
 Ser Val Lys Lys Lys Val Gln Arg Ser Val Glu Asp Gln Ser Val Leu
 180 185 190

gtt gca act tat gag ggt gaa cac aac cat cca atg cca tgg cag atc 742
 Val Ala Thr Tyr Glu Gly Glu His Asn His Pro Met Pro Ser Gln Ile
 195 200 205

gat tca aac aat ggc tta aac cgc cac atc tct cat ggt ggt tca gct 790
 Asp Ser Asn Asn Gly Leu Asn Arg His Ile Ser His Gly Gly Ser Ala
 210 215 220 225

tca aca ccc gtt gca gca aac aga aga agt agc ttg act gtg ccg gtg 838
 Ser Thr Pro Val Ala Ala Asn Arg Arg Ser Ser Leu Thr Val Pro Val
 230 235 240

act acc gta gat atg att gaa tgg aag aaa gtg acg agc cca acg tca 886
 Thr Thr Val Asp Met Ile Glu Ser Lys Lys Val Thr Ser Pro Thr Ser
 245 250 255

aga atc gat ttt ccc caa gtt cag aaa ctt ttg gtg gag caa atg gct 934
 Arg Ile Asp Phe Pro Gln Val Gln Lys Leu Leu Val Glu Gln Met Ala
 260 265 270

00704510.001300

tct tcc tta acc aaa gat cct aac ttt aca gca gct tta gca gca gct 982
 Ser Ser Leu Thr Lys Asp Pro Asn Phe Thr Ala Ala Leu Ala Ala Ala
 275 280 285

gtt acc gga aaa ttg tat caa cag aat cat acc gag aaa tagtttagct 1031
 Val Thr Gly Lys Leu Tyr Gln Gln Asn His Thr Glu Lys
 290 295 300

tcaaatccg ttagagtttt tagatttgaa tttgtcatga gtaagagaaa gagagtagat 1091

tataatccnt tgtgatactg aaaaaaaaaa aaaaaaaaaa 1130

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Leu Val Glu Glu Leu Asn Arg Val Ser Ala Glu Asn Lys Lys Leu Ser
 35 40 45

Glu Met Leu Thr Leu Met Cys Asp Asn Tyr Asn Val Leu Arg Lys Gln
 50 55 60

Leu Met Glu Tyr Val Asn Lys Ser Asn Ile Thr Glu Arg Asp Gln Ile
 65 70 75 80

Ser Pro Pro Lys Lys Arg Lys Ser Pro Ala Arg Glu Asp Ala Phe Ser
 85 90 95

Cys Ala Val Ile Gly Gly Val Ser Glu Ser Ser Ser Thr Asp Gln Asp
 100 105 110

Glu Tyr Leu Cys Lys Lys Gln Arg Glu Glu Thr Val Val Lys Glu Lys
 115 120 125

Val Ser Arg Val Tyr Tyr Lys Thr Glu Ala Ser Asp Thr Thr Leu Val
 130 135 140

Val Lys Asp Gly Tyr Gln Trp Arg Lys Tyr Gly Gln Lys Val Thr Arg
 145 150 155 160

Asp Asn Pro Ser Pro Arg Ala Tyr Phe Lys Cys Ala Cys Ala Pro Ser
 165 170 175

Cys Ser Val Lys Lys Lys Val Gln Arg Ser Val Glu Asp Gln Ser Val
 180 185 190

Ala Val Thr Gly Lys Leu Tyr Gln Gln Asn His Thr Glu Lys
290 295 300

aag aag cta acc gaa atg tta gca aga gtc tgt gag aag tac tat gct 246
Lys Lys Leu Thr Glu Met Leu Ala Arg Val Cys Glu Lys Tyr Tyr Ala
60 65 70

ctt aat aat ctt atg gag gag ttg cag agt cga aag agt cct gaa agt 294
 Leu Asn Asn Leu Met Glu Glu Leu Gln Ser Arg Lys Ser Pro Glu Ser
 75 80 85
 gtt aac ttt cag aac aaa cag cta acg ggg aaa cga aaa caa gaa ctt 342
 Val Asn Phe Gln Asn Lys Gln Leu Thr Gly Lys Arg Lys Gln Glu Leu
 90 95 100
 gat gag ttt gtt agc tcc cca att gga ctc agt ctc gga cca atc gag 390
 Asp Glu Phe Val Ser Ser Pro Ile Gly Leu Ser Leu Gly Pro Ile Glu
 105 110 115 120
 aac atc acc aac gat aaa gcg acg gtt tca acc gct tac ttt gct gct 438
 Asn Ile Thr Asn Asp Lys Lys Ala Thr Val Ser Thr Ala Tyr Phe Ala Ala
 125 130 135
 gag aag tct gac aca agc ttg act gtg aaa gat gga tat caa tgg agg 486
 Glu Lys Ser Asp Thr Ser Leu Thr Val Lys Asp Gly Tyr Gln Trp Arg
 140 145 150
 aaa tac ggg caa aag att acg aga gat aat cca tct cct aga gct tac 534
 Lys Tyr Gly Gln Lys Ile Thr Arg Asp Asn Pro Ser Pro Arg Ala Tyr
 155 160 165
 ttc aga tgc tgc ttt tca ccg tct tgt cta gtc aag aag aag gtg caa 582
 Phe Arg Cys Ser Phe Ser Pro Ser Cys Leu Val Lys Lys Lys Val Gln
 170 175 180
 cga agt gca gaa gat cca tct ttc ttg gta gcc act tac gaa ggg aca 630
 Arg Ser Ala Glu Asp Pro Ser Phe Leu Val Ala Thr Tyr Glu Gly Thr
 185 190 195 200
 cat aac cac acc gga cca cat gca agt gtg tcc agg aca gtg aaa ctt 678
 His Asn His Thr Gly Pro His Ala Ser Val Ser Arg Thr Val Lys Leu
 205 210 215
 gat cta gtt caa ggt ggg ctt gaa cca gtt gag gaa aag aaa gag aga 726
 Asp Leu Val Gln Gly Gly Leu Glu Pro Val Glu Glu Lys Lys Glu Arg
 220 225 230
 ggg acg att caa gag gtt ttg gtg caa caa atg gct tct tgc ttg acc 774
 Gly Thr Ile Gln Glu Val Leu Val Gln Gln Met Ala Ser Ser Leu Thr
 235 240 245
 aaa gat cct aag ttc act gca gct ctt gcg act gct att tcc ggg aga 822
 Lys Asp Pro Lys Phe Thr Ala Ala Leu Ala Thr Ala Ile Ser Gly Arg
 250 255 260
 ttg ata gag cat tca aga aca tgaaagtct ctagaacatg tatatttctg 873
 Leu Ile Glu His Ser Arg Thr
 265 270
 ttttgttcta ttttgttgct cattcctagt aaaaaggtaa agatttgttt gatcttgatt 933
 aggaggcata gatgtcaatt ttaatgtgtg tgtatataat tacatcaaat ctaagtatcc 993
 aaaaagggtc acccccattt tatcttatgn nnaaagannt ttganaaaaa aaaaaa 1049

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 20 25 30
 Lys Lys Trp Leu Val Lys Asp Glu Lys Arg Asn Met Leu Gln Asp Glu
 35 40 45
 Ile Asn Arg Val Asn Ser Glu Asn Lys Lys Leu Thr Glu Met Leu Ala
 50 55 60
 Arg Val Cys Glu Lys Tyr Tyr Ala Leu Asn Asn Leu Met Glu Glu Leu
 65 70 75 80
 Gln Ser Arg Lys Ser Pro Glu Ser Val Asn Phe Gln Asn Lys Gln Leu
 85 90 95
 Thr Gly Lys Arg Lys Gln Glu Leu Asp Glu Phe Val Ser Ser Pro Ile
 100 105 110
 Gly Leu Ser Leu Gly Pro Ile Glu Asn Ile Thr Asn Asp Lys Ala Thr
 115 120 125
 Val Ser Thr Ala Tyr Phe Ala Ala Glu Lys Ser Asp Thr Ser Leu Thr
 130 135 140
 Val Lys Asp Gly Tyr Gln Trp Arg Lys Tyr Gly Gln Lys Ile Thr Arg
 145 150 155 160
 Asp Asn Pro Ser Pro Arg Ala Tyr Phe Arg Cys Ser Phe Ser Pro Ser
 165 170 175
 Cys Leu Val Lys Lys Lys Val Gln Arg Ser Ala Glu Asp Pro Ser Phe
 180 185 190
 Leu Val Ala Thr Tyr Glu Gly Thr His Asn His Thr Gly Pro His Ala
 195 200 205
 Ser Val Ser Arg Thr Val Lys Leu Asp Leu Val Gln Gly Gly Leu Glu
 210 215 220
 Pro Val Glu Glu Lys Lys Glu Arg Gly Thr Ile Gln Glu Val Leu Val
 225 230 235 240
 Gln Gln Met Ala Ser Ser Leu Thr Lys Asp Pro Lys Phe Thr Ala Ala
 245 250 255

Leu Ala Thr Ala Ile Ser Gly Arg Leu Ile Glu His Ser Arg Thr
 260 265 270

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 <223> G1022

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 Met Thr Val Glu Leu Met Met
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agc agc tac agc ggc ggc gga gga gga ggt gat ggt ttt cct gca atc 103
 Ser Ser Tyr Ser Gly Gly Gly Gly Gly Asp Gly Phe Pro Ala Ile
 10 15 20

gcc gcg gcg gcg aaa atg gaa gat acc gct ttg aga gaa gct gct tct 151
 Ala Ala Ala Ala Lys Met Glu Asp Thr Ala Leu Arg Glu Ala Ala Ser
 25 30 35

gca ggg att cac ggt gtg gag gag ttt ctt aaa ctg atc ggt caa agt 199
 Ala Gly Ile His Gly Val Glu Glu Phe Leu Lys Leu Ile Gly Gln Ser
 40 45 50 55

caa caa cca acg gag aag agt cag acg gag ata acc gcg gtg act gac 247
 Gln Gln Pro Thr Glu Lys Ser Gln Thr Glu Ile Thr Ala Val Thr Asp
 60 65 70

gtc gcc gtt aac agc ttc aag aag gtc att tct cta ctc ggt aga tct 295
 Val Ala Val Asn Ser Phe Lys Lys Val Ile Ser Leu Leu Gly Arg Ser
 75 80 85

aga acc gga cac gct aga ttc aga cga gct ccc gcg tca acg caa acg 343
 Arg Thr Gly His Ala Arg Phe Arg Arg Ala Pro Ala Ser Thr Gln Thr
 90 95 100

ccg ttt aag caa acg ccg gtg gtt gag gag gag gtg gag gtg gag gag 391
 Pro Phe Lys Gln Thr Pro Val Val Glu Glu Glu Val Glu Val Glu Glu
 105 110 115

aag aag cca gaa aca agc tcc gtg tta aca aaa cag aaa aca gag caa 439
 Lys Lys Pro Glu Thr Ser Ser Val Leu Thr Lys Gln Lys Thr Glu Gln
 120 125 130 135

tat cac ggt ggt gga tct gcg ttt aga gtt tat tgt cca aca cca att 487
 Tyr His Gly Gly Ser Ala Phe Arg Val Tyr Cys Pro Thr Pro Ile
 140 145 150

cat cgt cgt cct cct cta tca cac aat aac aac aac aat cag aat caa 535
 His Arg Arg Pro Pro Leu Ser His Asn Asn Asn Asn Gln Asn Gln
 155 160 165

aca aag aac ggt tct tct tca tct cct ccg atg ctc gca aac gga 583
 Thr Lys Asn Gly Ser Ser Ser Ser Pro Pro Met Leu Ala Asn Gly
 170 175 180

gca ccg tca acg ata aac ttt gcg ccg tca cca cca gtc tca gcg acg 631
 Ala Pro Ser Thr Ile Asn Phe Ala Pro Ser Pro Val Ser Ala Thr
 185 190 195

aac tca ttc atg tct tct cat aga tgt gac acc gat agt act cac atg 679
 Asn Ser Phe Met Ser Ser His Arg Cys Asp Thr Asp Ser Thr His Met
 200 205 210 215

tca tca gga ttc gag ttc act aac cca tct cag ctc tct ggt tct aga 727
 Ser Ser Gly Phe Glu Phe Thr Asn Pro Ser Gln Leu Ser Gly Ser Arg
 220 225 230

ggt aaa cct cct tta tca tca gct tct ttg aag aga aga tgt aat tca 775
 Gly Lys Pro Pro Leu Ser Ser Ala Ser Leu Lys Arg Arg Cys Asn Ser
 235 240 245

tct ccc tca agc cgt tgc cat tgc tcc aag aaa agg aaa tca aga gta 823
 Ser Pro Ser Ser Arg Cys His Cys Ser Lys Lys Arg Lys Ser Arg Val
 250 255 260

aaa aga gtg att aga gtt cca gca gta agt agc aaa atg gct gat ata 871
 Lys Arg Val Ile Arg Val Pro Ala Val Ser Ser Lys Met Ala Asp Ile
 265 270 275

cca tca gat gag ttt tca tgg aga aaa tat ggt caa aaa cca atc aaa 919
 Pro Ser Asp Glu Phe Ser Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys
 280 285 290 295

ggc tct cct cat cct ccg gga tat tac aag tgc agc agt gta aga ggt 967
 Gly Ser Pro His Pro Arg Gly Tyr Tyr Lys Cys Ser Ser Val Arg Gly
 300 305 310

tgt ccg gcg cgt aag cat gtg gag cgt gca cta gat gat gcg atg atg 1015
 Cys Pro Ala Arg Lys His Val Glu Arg Ala Leu Asp Asp Ala Met Met
 315 320 325

cta atc gtg acg tac gaa gga gac cac aac cat gct ttg gtt ctc gag 1063
 Leu Ile Val Thr Tyr Glu Gly Asp His Asn His Ala Leu Val Leu Glu
 330 335 340

acg acg acg atg aat cat gac aaa act ctt tagtttctcg agtttgaggg 1113
 Thr Thr Thr Met Asn His Asp Lys Thr Leu
 345 350

gaactgtctg tgtgtgacca ctatccagat tagtcaacga cagagtgggc ccgcaactgca 1173

cttttttatt cttttttttt tgaaaagcctt ttgctttatc tttctttttg attggaggagaa 1233

atagaggggag gggagataaa gacgagagag gaacgttgtg gatcttgatg gaagtgaat 1293

catgtgaatg tccttttctg tttattttatt tctaggataa tatatatatta gtgcactatt 1353

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<220>
 <223> G1022

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 Ala Leu Arg Glu Ala Ala Ser Ala Gly Ile His Gly Val Glu Glu Phe
 35 40 45
 Leu Lys Leu Ile Gly Gln Ser Gln Gln Pro Thr Glu Lys Ser Gln Thr
 50 55 60
 Glu Ile Thr Ala Val Thr Asp Val Ala Val Asn Ser Phe Lys Lys Val
 65 70 75 80
 Ile Ser Leu Leu Gly Arg Ser Arg Thr Gly His Ala Arg Phe Arg Arg
 85 90 95
 Ala Pro Ala Ser Thr Gln Thr Pro Phe Lys Gln Thr Pro Val Val Glu
 100 105 110
 Glu Glu Val Glu Val Glu Glu Lys Lys Pro Glu Thr Ser Ser Val Leu
 115 120 125
 Thr Lys Gln Lys Thr Glu Gln Tyr His Gly Gly Ser Ala Phe Arg
 130 135 140
 Val Tyr Cys Pro Thr Pro Ile His Arg Arg Pro Pro Leu Ser His Asn
 145 150 155 160
 Asn Asn Asn Asn Gln Asn Gln Thr Lys Asn Gly Ser Ser Ser Ser Ser
 165 170 175
 Pro Pro Met Leu Ala Asn Gly Ala Pro Ser Thr Ile Asn Phe Ala Pro
 180 185 190
 Ser Pro Pro Val Ser Ala Thr Asn Ser Phe Met Ser Ser His Arg Cys
 195 200 205
 Asp Thr Asp Ser Thr His Met Ser Ser Gly Phe Glu Phe Thr Asn Pro
 210 215 220
 Ser Gln Leu Ser Gly Ser Arg Gly Lys Pro Pro Leu Ser Ser Ala Ser
 225 230 235 240
 Leu Lys Arg Arg Cys Asn Ser Ser Pro Ser Ser Arg Cys His Cys Ser
 245 250 255

Lys Lys Arg Lys Ser Arg Val Lys Arg Val Ile Arg Val Pro Ala Val
 260 265 270
 Ser Ser Lys Met Ala Asp Ile Pro Ser Asp Glu Phe Ser Trp Arg Lys
 275 280 285
 Tyr Gly Gln Lys Pro Ile Lys Gly Ser Pro His Pro Arg Gly Tyr Tyr
 290 295 300
 Lys Cys Ser Ser Val Arg Gly Cys Pro Ala Arg Lys His Val Glu Arg
 305 310 315 320
 Ala Leu Asp Asp Ala Met Met Leu Ile Val Thr Tyr Glu Gly Asp His
 325 330 335
 Asn His Ala Leu Val Leu Glu Thr Thr Thr Met Asn His Asp Lys Thr
 340 345 350

Leu

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 <211> 1099
 <212> DNA
 <213> Arabidopsis thaliana

<220>
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 <222> (43)..(924)
 <223> G1043

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 aaa gca aaa aag ctt aaa gtt atg aac caa ctc gtt gaa ggc cat gac 102
 Lys Ala Lys Lys Leu Lys Val Met Asn Gln Leu Val Glu Gly His Asp
 5 10 15 20
 tta aca act cag ctt cag caa ctc ctc tct caa ccc ggg tcc ggt cta 150
 Leu Thr Thr Gln Leu Gln Gln Leu Leu Ser Gln Pro Gly Ser Gly Leu
 25 30 35
 gag gat cta gtg gct aaa atc tta gtg tgt ttc aat aac acc atc tcc 198
 Glu Asp Leu Val Ala Lys Ile Leu Val Cys Phe Asn Asn Thr Ile Ser
 40 45 50
 gtt ctt gat acc ttc gaa ccc atc tcc tcc tcc tca tcc etc gcc gcc 246
 Val Leu Asp Thr Phe Glu Pro Ile Ser Ser Ser Ser Ser Leu Ala Ala
 55 60 65
 gtt gag gga tct caa aat gct tca tgt gat aac gac ggc aag ttt gaa 294
 Val Glu Gly Ser Gln Asn Ala Ser Cys Asp Asn Asp Gly Lys Phe Glu
 70 75 80

gat tcc ggc gat agt cgg aaa aga ttg gga ccc gtt aag ggt aaa aga	342
Asp Ser Gly Asp Ser Arg Lys Arg Leu Gly Pro Val Lys Gly Lys Arg	
85 90 95 100	
gga tgc tac aaa aga aaa aag aga tcg gag acg tgt act ata gag tcg	390
Gly Cys Tyr Lys Arg Lys Lys Arg Ser Glu Thr Cys Thr Ile Glu Ser	
105 110 115	
act ata ctt gag gac gca ttt tct tgg agg aaa tat gga caa aag gag	438
Thr Ile Leu Glu Asp Ala Phe Ser Trp Arg Lys Tyr Gly Gln Lys Glu	
120 125 130	
att ctt aat gcc aaa ttc cca aga agt tac ttt aga tgc aca cac aag	486
Ile Leu Asn Ala Lys Phe Pro Arg Ser Tyr Phe Arg Cys Thr His Lys	
135 140 145	
tat acc caa ggg tgc aag gca aca aag caa gtc cag aag gtt gag ctc	534
Tyr Thr Gln Gly Cys Lys Ala Thr Lys Gln Val Gln Lys Val Glu Leu	
150 155 160	
gaa ccc aag atg ttc agt atc aca tac ata gga aac cac acg tgt aac	582
Glu Pro Lys Met Phe Ser Ile Thr Tyr Ile Gly Asn His Thr Cys Asn	
165 170 175 180	
acc aac gca gaa act ccc aag agc aag act tgt gac cat cat gat gag	630
Thr Asn Ala Glu Thr Pro Lys Ser Lys Thr Cys Asp His His Asp Glu	
185 190 195	
atc ttc atg gat tcc gaa gat cac aag agt cct agt tta tct acc tca	678
Ile Phe Met Asp Ser Glu Asp His Lys Ser Pro Ser Leu Ser Thr Ser	
200 205 210	
atg aag gaa gaa gac aat cct cat cgt cat cat ggt tcg tcc acg gag	726
Met Lys Glu Glu Asp Asn Pro His Arg His His Gly Ser Ser Thr Glu	
215 220 225	
aat gac ttg tca ttg gtg tgg cca gaa atg gtt ttc gaa gaa gat tat	774
Asn Asp Leu Ser Leu Val Trp Pro Glu Met Val Phe Glu Glu Asp Tyr	
230 235 240	
cat cat cag gcc agt tac gtc aat ggg aaa acg agt aca tct atc gat	822
His His Gln Ala Ser Tyr Val Asn Gly Lys Thr Ser Thr Ser Ile Asp	
245 250 255 260	
gtt ttg ggt tct cag gat ctc atg gtg ttt gga ggt ggc ggc gat ttc	870
Val Leu Gly Ser Gln Asp Leu Met Val Phe Gly Gly Gly Gly Asp Phe	
265 270 275	
gag ttt agc gaa aat gag cac ttc tct atc ttc agt tca tgt tcg aat	918
Glu Phe Ser Glu Asn Glu His Phe Ser Ile Phe Ser Ser Cys Ser Asn	
280 285 290	
cta tct tgagtttacc actactatag gactaagacc atgagtttta atcattaatt	974
Leu Ser	
aggccatgta gagggtgaaaa catataatac atattttgcc cttttctcta atgagtgat	1034
gtactgtaca tatagtacta taaataaaac tcttgctgga ttaaaacaaa aaaaaaaaaa	1094

aaaaa

1099

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 <212> PRT
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 20 25 30
 Gly Ser Gly Leu Glu Asp Leu Val Ala Lys Ile Leu Val Cys Phe Asn
 35 40 45
 Asn Thr Ile Ser Val Leu Asp Thr Phe Glu Pro Ile Ser Ser Ser Ser
 50 55 60
 Ser Leu Ala Ala Val Glu Gly Ser Gln Asn Ala Ser Cys Asp Asn Asp
 65 70 75 80
 Gly Lys Phe Glu Asp Ser Gly Asp Ser Arg Lys Arg Leu Gly Pro Val
 85 90 95
 Lys Gly Lys Arg Gly Cys Tyr Lys Arg Lys Lys Arg Ser Glu Thr Cys
 100 105 110
 Thr Ile Glu Ser Thr Ile Leu Glu Asp Ala Phe Ser Trp Arg Lys Tyr
 115 120 125
 Gly Gln Lys Glu Ile Leu Asn Ala Lys Phe Pro Arg Ser Tyr Phe Arg
 130 135 140
 Cys Thr His Lys Tyr Thr Gln Gly Cys Lys Ala Thr Lys Gln Val Gln
 145 150 155 160
 Lys Val Glu Leu Glu Pro Lys Met Phe Ser Ile Thr Tyr Ile Gly Asn
 165 170 175
 His Thr Cys Asn Thr Asn Ala Glu Thr Pro Lys Ser Lys Thr Cys Asp
 180 185 190
 His His Asp Glu Ile Phe Met Asp Ser Glu Asp His Lys Ser Pro Ser
 195 200 205
 Leu Ser Thr Ser Met Lys Glu Glu Asp Asn Pro His Arg His His Gly
 210 215 220
 Ser Ser Thr Glu Asn Asp Leu Ser Leu Val Trp Pro Glu Met Val Phe
 225 230 235 240

Glu Glu Asp Tyr His His Gln Ala Ser Tyr Val Asn Gly Lys Thr Ser
 245 250 255

Thr Ser Ile Asp Val Leu Gly Ser Gln Asp Leu Met Val Phe Gly Gly
 260 265 270

Gly Gly Asp Phe Glu Phe Ser Glu Asn Glu His Phe Ser Ile Phe Ser
 275 280 285

Ser Cys Ser Asn Leu Ser
 290

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 <212> DNA
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<220>
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 <222> (49)..(1038)
 <223> g1091

<400> 93
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ggt gaa gct gct aac aga tca gct ata gaa agc tgt cat gga gtg tta 105
 Val Glu Ala Ala Asn Arg Ser Ala Ile Glu Ser Cys His Gly Val Leu
 5 10 15

aat ctg ttg tca caa cga acc agt gat ccc aaa tcc tta acg gtt gaa 153
 Asn Leu Leu Ser Gln Arg Thr Ser Asp Pro Lys Ser Leu Thr Val Glu
 20 25 30 35

aca gga gaa gta gtt tcc aag ttc aaa aga gta gct tct ctg tta act 201
 Thr Gly Glu Val Val Ser Lys Phe Lys Arg Val Ala Ser Leu Leu Thr
 40 45 50

aga ggg tta ggc cat gga aag ttt agg agt acc aac aag ttt agg tca 249
 Arg Gly Leu Gly His Gly Lys Phe Arg Ser Thr Asn Lys Phe Arg Ser
 55 60 65

tct ttt cct caa cac atc ttc tta gag agt cct att tgc tgc ggt aat 297
 Ser Phe Pro Gln His Ile Phe Leu Glu Ser Pro Ile Cys Gly Asn
 70 75 80

gat cta agt ggt gat tac act caa gtt ctt gca cca gag cca ctt cag 345
 Asp Leu Ser Gly Asp Tyr Thr Gln Val Leu Ala Pro Glu Pro Leu Gln
 85 90 95

atg gtt cca gct tct gct gtt tat aat gaa atg gag cca aaa cac caa 393
 Met Val Pro Ala Ser Ala Val Tyr Asn Glu Met Glu Pro Lys His Gln
 100 105 110 115

agctctgatt tgcaattgta tatttccact ctgacagaag ttataagagc acttgtgaac 1188
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 tttcttcaaa aaaaaaaaaa aaaaaaaaaa a 1279

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 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G1091

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 Thr Val Glu Thr Gly Glu Val Val Ser Lys Phe Lys Arg Val Ala Ser
 35 40 45
 Leu Leu Thr Arg Gly Leu Gly His Gly Lys Phe Arg Ser Thr Asn Lys
 50 55 60
 Phe Arg Ser Ser Phe Pro Gln His Ile Phe Leu Glu Ser Pro Ile Cys
 65 70 75 80
 Cys Gly Asn Asp Leu Ser Gly Asp Tyr Thr Gln Val Leu Ala Pro Glu
 85 90 95
 Pro Leu Gln Met Val Pro Ala Ser Ala Val Tyr Asn Glu Met Glu Pro
 100 105 110
 Lys His Gln Leu Gly His Pro Ser Leu Met Leu Ser His Lys Met Cys
 115 120 125
 Val Asp Lys Ser Phe Leu Glu Leu Lys Pro Pro Pro Phe Arg Ala Pro
 130 135 140
 Tyr Gln Leu Ile His Asn His Gln Gln Ile Ala Tyr Ser Arg Ser Asn
 145 150 155 160
 Ser Gly Val Asn Leu Lys Phe Asp Gly Ser Gly Ser Ser Cys Tyr Thr
 165 170 175
 Pro Ser Val Ser Asn Gly Ser Arg Ser Phe Val Ser Ser Leu Ser Met
 180 185 190
 Asp Ala Ser Val Thr Asp Tyr Asp Arg Asn Ser Phe His Leu Thr Gly
 195 200 205
 Leu Ser Arg Gly Ser Asp Gln Gln His Thr Arg Lys Met Cys Ser Gly
 210 215 220

Ser Leu Lys Cys Gly Ser Arg Ser Lys Cys His Cys Ser Lys Lys Arg
 225 230 235 240

Lys Leu Arg Val Lys Arg Ser Ile Lys Val Pro Ala Ile Ser Asn Lys
 245 250 255

Ile Ala Asp Ile Pro Pro Asp Glu Tyr Ser Trp Arg Lys Tyr Gly Gln
 260 265 270

Lys Pro Ile Lys Gly Ser Pro His Pro Arg Gly Tyr Tyr Lys Cys Ser
 275 280 285

Ser Val Arg Gly Cys Pro Ala Arg Lys His Val Glu Arg Cys Ile Asp
 290 295 300

Glu Thr Ser Met Leu Ile Val Thr Tyr Glu Gly Glu His Asn His Ser
 305 310 315 320

Arg Ile Leu Ser Ser Gln Ser Ala His Thr
 325 330

<210> 95
 <211> 2601

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (143)..(2452)

<223> G837

<400> 95

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aagtttcatt ctttggggag atctgaggca accctttttc tctggtgcat gtgactaggg 120

attgtgccgt gggtttagga tc atg gca atg ggg aag tat tct cgt gta gac 172
 Met Ala Met Gly Lys Tyr Ser Arg Val Asp
 1 5 10

ggg aag aag tca tgc gga tat ggc tta acc att acc atc gtt tta att 220
 Gly Lys Lys Ser Ser Gly Tyr Gly Leu Thr Ile Thr Ile Val Leu Ile
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 Val Ile Gln Phe Ile Asn Pro Lys Val Gln Ala Ser Ile Ala Ala Asn
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 Leu Leu Gly Pro Asp Ser Pro Ile Asp Ala Tyr Ser Cys Asp His Phe
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Cys Pro Arg Cys Asn Ser Leu Asn Thr Lys Phe Cys Tyr Tyr Asn Asn
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Tyr Ser Leu Thr Gln Pro Arg Tyr Phe Cys Lys Asp Cys Arg Arg Tyr
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Trp	Leu	Asn	Val	Arg	Gln	Thr	Thr	Glu	Pro	Gly	Leu	Asp	Ala	Ser	Val					
	80					85					90									
ata	gaa	acg	ttt	cca	acg	ttt	cct	tac	tct	aca	gtg	aag	acg	ttg	agg					459
Ile	Glu	Thr	Phe	Pro	Thr	Phe	Pro	Tyr	Ser	Thr	Val	Lys	Thr	Leu	Arg					
95					100					105					110					
atc	ggt	aaa	gaa	gct	ttg	gag	tgt	ccc	ggt	tgt	ctc	aac	gag	ttc	gag					507
Ile	Gly	Lys	Glu	Ala	Leu	Glu	Cys	Pro	Val	Cys	Leu	Asn	Glu	Phe	Glu					
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Asp	Asp	Glu	Thr	Leu	Arg	Leu	Ile	Pro	Gln	Cys	Cys	His	Val	Phe	His					
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Pro	Gly	Cys	Ile	Asp	Ala	Trp	Leu	Arg	Ser	Gln	Thr	Thr	Tyr	Cys	Pro	Leu				
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tgc	cga	gcc	aat	ctc	gtt	cct	gta	ccg	ggt	gag	tct	gtt	tct	tcg	gag					651
Cys	Arg	Ala	Asn																	

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 Met Ser Thr Gly Trp Lys Leu Ala Glu Leu Tyr Ser Pro Ala Ser Ser
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 Pro Gly Gln Pro Glu Glu Asn Leu Asp Arg Tyr Thr Leu Arg Leu Pro
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 Gln Glu Ile His Asp Gln Leu Val Asn Ser Ser Leu Gly Lys Gln Gly
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 Ser Lys Gly Gln Leu Ala Leu Pro Gln Glu Arg Ser Ser Val Arg Gly
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Asp Asn Arg Lys Arg Val Leu Thr Ser Pro Asp Glu Arg Leu Ile Asp
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 225 230 235 240

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 275 280 285

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Gly Met Pro Tyr His Lys Ser Cys Phe Arg Cys Thr His Cys Lys Gly
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Thr Leu Gln Met Ser Asn Tyr Ser Ser Met Asp Gly Val Leu Tyr Cys
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Cys Glu Lys Thr Val Tyr Pro Leu Glu Lys Ile Gln Met Glu Gly Glu
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Cys Phe His Lys Thr Cys Phe Arg Cys Ala His Gly Cys Thr Leu
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Thr His Ser Ser Tyr Ala Ser Leu Asp Ser Val Leu Tyr Cys Arg His
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65 70 75 80

Thr Glu Lys Pro Glu Leu Thr Arg Thr Pro Ser Lys Ile Ser Ser Ile
85 90 95

Phe Cys Gly Thr Gln Asp Lys Cys Ala Ala Cys Glu Lys Thr Val Tyr
100 105 110

Pro Leu Glu Lys Ile Gln Met Glu Gly Glu Cys Phe His Lys Thr Cys
115 120 125

Phe Arg Cys Ala His Gly Gly Cys Thr Leu Thr His Ser Ser Tyr Ala
130 135 140

Ser Leu Asp Ser Val Leu Tyr Cys Arg His His Phe Asn Gln Leu Phe
145 150 155 160

Met Glu Lys Gly Asn Tyr Ala His Val Leu Gln Ala Ala Asn His Arg
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Phe Ile Thr Glu Leu Gln Ile Pro Gly Tyr Ile Leu Lys Ile Leu Tyr
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Val Ile Gly Phe Phe Arg Asp Met Val Asp Ala Leu Cys Pro Tyr Ile
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Gly Leu Pro Ser Phe Leu Asp His Asn Glu Thr Ser Gly Pro Asp Pro
40 45 50

acc cga cac gct ctc tct acg tca gcg agt ctt gct aac gag ttg atc 246
Thr Arg His Ala Leu Ser Thr Ser Ala Ser Leu Ala Asn Glu Leu Ile
55 60 65 70

ccg gtg gtt cgg ttc tcg gat ctt ccg acc gat ccg gaa gat tgt tgt 294
Pro Val Val Arg Phe Ser Asp Leu Pro Thr Asp Pro Glu Asp Cys Cys
75 80 85

acg gtt tgt ttg tca gat ttt gag tcc gac gat aag gtt agg cag cta 342
Thr Val Cys Leu Ser Asp Phe Glu Ser Asp Asp Lys Val Arg Gln Leu
90 95 100

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Pro Lys Cys Gly His Val Phe His His His Cys Leu Asp Arg Trp Ile
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gtt gac tac aac aag atg aaa tgt ccg gtt tgt cgg cac cgg ttc tta 438
Val Asp Tyr Asn Lys Met Lys Cys Pro Val Cys Arg His Arg Phe Leu
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Pro Lys Glu Lys Tyr Thr Gln Cys Asp Trp Gly Ser Gly Ser Asp Trp
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Glu Thr Leu Leu Gly Arg Gly Leu Asp Thr Glu Ser Tyr Ala Met Glu
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Glu Leu Gly Leu Ser Asn Ser Glu Met Phe Lys Ile Glu Lys Asp Glu
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Ile Glu Glu Glu Val Glu Glu Ile Lys Ala Met Ser Met Asp Ile Phe
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Cys Pro Arg Cys Asp Ser Thr Asn Thr Lys Phe Cys Tyr Tyr Asn Asn	
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Trp Thr Lys Gly Gly Thr Leu Arg Asn Ile Pro Val Gly Gly Gly Cys	
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Gln Met Asn Gly Glu Ser Phe Gly Met Met Ala Ile Gly Gly Gly	
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 Gly Lys Val Phe Ser Ala Ala Gly Phe Asn Gly Tyr Ser Asn Asn Glu
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 Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu Gly Val Lys Glu Glu Glu
 160 165 170 175
 gtt cac aag acg gat tcg att cct tcg tct cct ctg cag ttt cta gaa 575
 Val His Lys Thr Asp Ser Ile Pro Ser Ser Pro Leu Gln Phe Leu Glu
 180 185 190
 cat tcc tct ggt ttt aac tac cgg cga agc ttc act gac ctc cgt gac 623
 His Ser Ser Gly Phe Asn Tyr Arg Arg Ser Phe Thr Asp Leu Arg Asp
 195 200 205
 ctt cta ccg aat tcc acc gtt gtc gag gct gga tct tcc gat agt tgc 671
 Leu Leu Pro Asn Ser Thr Val Val Glu Ala Gly Ser Ser Asp Ser Cys
 210 215 220
 gat tca agc gcc gtt ctt aac gac gaa aca agt tct gat aac gga aga 719
 Asp Ser Ser Ala Val Leu Asn Asp Glu Thr Ser Ser Asp Asn Gly Arg
 225 230 235
 ttg acg ccg cct gtg acg gtt act ggc ggg agt ttc tta cag ttt gtg 767
 Leu Thr Pro Pro Val Thr Val Thr Gly Gly Ser Phe Leu Gln Phe Val
 240 245 250 255
 aaa aca gag caa aca gag gat cac gag gat ttt cta agc ggt gaa gaa 815
 Lys Thr Glu Gln Thr Glu Asp His Glu Asp Phe Leu Ser Gly Glu Glu
 260 265 270
 gct tgt ggt ttc ttc tcc gat gaa cag ccg ccg tca ctt cat tgg tac 863
 Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro Pro Ser Leu His Trp Tyr
 275 280 285
 tct gct tca gat cat tgg act tgagaattgt ttatcaaatt ggtgctctgt 914
 Ser Ala Ser Asp His Trp Thr
 290
 ttagtctcaa tgggaaacaa gagaagaggg caaaggtgga ataattgata aataaggatt 974

aaggatgaag gggattatta aattaaatcc gcgggagaag ttaattttgg gtttaagatt 1034
 gtaatggctc ttcattgtaat taacgatgct gagaggggct ttcacagaaa taggaatcaa 1094
 tggggacact ctgatatgaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1154
 aaa 1157

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 <211> 294
 <212> PRT
 <213> Arabidopsis thaliana

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 <223> G699

<400> 126
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 35 40 45
 Gly Asn His His His Met Gly Leu Ser Glu Lys Lys Arg Arg Leu Lys
 50 55 60
 Val Asp Gln Val Lys Ala Leu Glu Lys Asn Phe Glu Leu Glu Asn Lys
 65 70 75 80
 Leu Glu Pro Glu Arg Lys Thr Lys Leu Ala Gln Glu Leu Gly Leu Gln
 85 90 95
 Pro Arg Gln Val Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp Lys
 100 105 110
 Thr Lys Gln Leu Glu Lys Asp Tyr Gly Val Leu Lys Gly Gln Tyr Asp
 115 120 125
 Ser Leu Arg His Asn Phe Asp Ser Leu Arg Arg Asp Asn Asp Ser Leu
 130 135 140
 Leu Gln Glu Ile Ser Lys Ile Lys Ala Lys Val Asn Gly Glu Glu Asp
 145 150 155 160
 Asn Asn Asn Asn Lys Ala Ile Thr Glu Gly Val Lys Glu Glu Glu Val
 165 170 175
 His Lys Thr Asp Ser Ile Pro Ser Ser Pro Leu Gln Phe Leu Glu His
 180 185 190
 Ser Ser Gly Phe Asn Tyr Arg Arg Ser Phe Thr Asp Leu Arg Asp Leu
 195 200 205

Leu Pro Asn Ser Thr Val Val Glu Ala Gly Ser Ser Asp Ser Cys Asp
210 215 220

Ser Ser Ala Val Leu Asn Asp Glu Thr Ser Ser Asp Asn Gly Arg Leu
225 230 235 240

Thr Pro Pro Val Thr Val Thr Gly Gly Ser Phe Leu Gln Phe Val Lys
245 250 255

Thr Glu Gln Thr Glu Asp His Glu Asp Phe Leu Ser Gly Glu Glu Ala
260 265 270

Cys Gly Phe Phe Ser Asp Glu Gln Pro Pro Ser Leu His Trp Tyr Ser
275 280 285

Ala Ser Asp His Trp Thr
290

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<211> 1221

<212> DNA

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<220>

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<222> (162)..(1010)

<223> G964

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ttcctgaaac tgttgagttc ttgtgaaagg aaataaaaaa c atg atg atg ggc aaa 176
Met Met Met Gly Lys
1 5

gaa gat cta ggt ttg agc cta agc tta ggg ttt tca caa aat cac aat 224
Glu Asp Leu Gly Leu Ser Leu Ser Leu Gly Phe Ser Gln Asn His Asn
10 15 20

cct ctt cag atg aat ctg aat cct aac tct tca tta tca aac aat ctc 272
Pro Leu Gln Met Asn Leu Asn Pro Asn Ser Ser Leu Ser Asn Asn Leu
25 30 35

cag aga ctc cca tgg aac caa aca ttc gat cct aca tca gat ctt cgc 320
Gln Arg Leu Pro Trp Asn Gln Thr Phe Asp Pro Thr Ser Asp Leu Arg
40 45 50

aag ata gac gtg aac agt ttt cca tca acg gtt aac tgc gag gaa gac 368
Lys Ile Asp Val Asn Ser Phe Pro Ser Thr Val Asn Cys Glu Glu Asp
55 60 65

aca gga gtt tcg tca cca aac agt acg atc tca agc acc att agc ggg 416
Thr Gly Val Ser Ser Pro Asn Ser Thr Ile Ser Ser Thr Ile Ser Gly
70 75 80 85

aag aga agt gag aga gaa gga atc tcc gga acc ggc gtt ggc tcc ggc 464
Lys Arg Ser Glu Arg Glu Gly Ile Ser Gly Thr Gly Val Gly Ser Gly
90 95 100

gac gat cac gac gag atc act ccg gat cga ggg tac tca cgt gga acc 512
Asp Asp His Asp Glu Ile Thr Pro Asp Arg Gly Tyr Ser Arg Gly Thr
105 110 115

tca gat gaa gaa gaa gac ggg ggc gaa acg tcg agg aag aag ctc agg 560
Ser Asp Glu Glu Glu Asp Gly Gly Glu Thr Ser Arg Lys Lys Leu Arg
120 125 130

tta tca aaa gat cag tct gct ttt ctc gaa gag act ttc aaa gaa cac 608
Leu Ser Lys Asp Gln Ser Ala Phe Leu Glu Glu Thr Phe Lys Glu His
135 140 145

aac act ctc aat ccc aaa cag aag cta gct ttg gct aag aag ctg aac 656
Asn Thr Leu Asn Pro Lys Gln Lys Leu Ala Leu Ala Lys Lys Leu Asn
150 155 160 165

ttg acg gca aga caa gtg gaa gtg tgg ttc caa aac aga aga gct aga 704
Leu Thr Ala Arg Gln Val Glu Val Trp Phe Gln Asn Arg Arg Ala Arg
170 175 180

acc aag tta aag caa acg gag gta gat tgc gaa tac ttg aaa cgg tgc 752
Thr Lys Leu Lys Gln Thr Glu Val Asp Cys Glu Tyr Leu Lys Arg Cys
185 190 195

gta gag aag cta acg gaa gag aac cgg aga ctt cag aaa gag gct atg 800
Val Glu Lys Leu Thr Glu Glu Asn Arg Arg Leu Gln Lys Glu Ala Met
200 205 210

gag ctt cga act ctc aag ctg tct cca caa ttc tac ggt cag atg act 848
Glu Leu Arg Thr Leu Lys Leu Ser Pro Gln Phe Tyr Gly Gln Met Thr
215 220 225

cca cca act aca ctc atc atg tgt cct tgc tgc gag cgt gta gct ggt 896
Pro Pro Thr Thr Leu Ile Met Cys Pro Ser Cys Glu Arg Val Ala Gly
230 235 240 245

cca tca tca tgc aac cat cac cac aat cac agg cgg gtt tgc att aac 944
Pro Ser Ser Ser Asn His His His Asn His Arg Pro Val Ser Ile Asn
250 255 260

ccg tgg att gct tgt gct ggt cag gtg gct cat ggg ctg aat ttt gaa 992
Pro Trp Ile Ala Cys Ala Gly Gln Val Ala His Gly Leu Asn Phe Glu
265 270 275

gcc ttg cgt cca cga tgc taatttttag tgggtggggga aggggtgtttt 1040
Ala Leu Arg Pro Arg Ser
280

gggttttttc attatcgtaa tatagtctat ctgtgtgggg tcattgtaatt tttggatgat 1100

tggccttctc atgaactagt catatgtatg atgcaacctt aaaaaatattt caagtagcaa 1160

aacttaatta caaacttgct atattaacca aaaattatga aaaaaaaaaa aaaaaaaaaa 1220

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1221

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 Leu Ser Asn Asn Leu Gln Arg Leu Pro Trp Asn Gln Thr Phe Asp Pro
 35 40 45
 Thr Ser Asp Leu Arg Lys Ile Asp Val Asn Ser Phe Pro Ser Thr Val
 50 55 60
 Asn Cys Glu Glu Asp Thr Gly Val Ser Ser Pro Asn Ser Thr Ile Ser
 65 70 75 80
 Ser Thr Ile Ser Gly Lys Arg Ser Glu Arg Glu Gly Ile Ser Gly Thr
 85 90 95
 Gly Val Gly Ser Gly Asp Asp His Asp Glu Ile Thr Pro Asp Arg Gly
 100 105 110
 Tyr Ser Arg Gly Thr Ser Asp Glu Glu Asp Gly Gly Glu Thr Ser
 115 120 125
 Arg Lys Lys Leu Arg Leu Ser Lys Asp Gln Ser Ala Phe Leu Glu Glu
 130 135 140
 Thr Phe Lys Glu His Asn Thr Leu Asn Pro Lys Gln Lys Leu Ala Leu
 145 150 155 160
 Ala Lys Lys Leu Asn Leu Thr Ala Arg Gln Val Glu Val Trp Phe Gln
 165 170 175
 Asn Arg Arg Ala Arg Thr Lys Leu Lys Gln Thr Glu Val Asp Cys Glu
 180 185 190
 Tyr Leu Lys Arg Cys Val Glu Lys Leu Thr Glu Glu Asn Arg Arg Leu
 195 200 205
 Gln Lys Glu Ala Met Glu Leu Arg Thr Leu Lys Leu Ser Pro Gln Phe
 210 215 220
 Tyr Gly Gln Met Thr Pro Pro Thr Thr Leu Ile Met Cys Pro Ser Cys
 225 230 235 240

Glu Arg Val Ala Gly Pro Ser Ser Ser Asn His His His Asn His Arg
245 250 255

Pro Val Ser Ile Asn Pro Trp Ile Ala Cys Ala Gly Gln Val Ala His
260 265 270

Gly Leu Asn Phe Glu Ala Leu Arg Pro Arg Ser
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<210> 129

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<222> (76)..(882)

<223> 1334

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Met Gln Thr Glu Glu Leu Leu Ser Pro Pro Gln Thr
1 5 10

cct tgg tgg aat gct ttt gga tct cag cag ttg act aca gag agc ctt 159
Pro Trp Trp Asn Ala Phe Gly Ser Gln Pro Leu Thr Thr Glu Ser Leu
15 20 25

tcc ggc gaa gct tct gat tca ttc acc gga gtt aag gca gtt act acg 207
Ser Gly Glu Ala Ser Asp Ser Phe Thr Gly Val Lys Ala Val Thr Thr
30 35 40

gag gca gaa caa ggt gtg gtg gat aaa caa act tct aca act ctc ttc 255
Glu Ala Glu Gln Gly Val Val Asp Lys Gln Thr Ser Thr Thr Leu Phe
45 50 55 60

act ttc tca cct ggt ggt gaa aag agt tca aga gat gtg cca aag cct 303
Thr Phe Ser Pro Gly Gly Glu Lys Ser Ser Arg Asp Val Pro Lys Pro
65 70 75

cat gtt gct ttc gcg atg caa tca gct tgc ttc gag ttt gga ttt gct 351
His Val Ala Phe Ala Met Gln Ser Ala Cys Phe Glu Phe Gly Phe Ala
80 85 90

cag cca atg atg tac aca aag cat cct cat gtt gaa caa tac tat gga 399
Gln Pro Met Met Tyr Thr Lys His Pro His Val Glu Gln Tyr Tyr Gly
95 100 105

gtt gtt tca gca tac gga tct cag agg tct tcg ggc cga gta atg att 447
Val Val Ser Ala Tyr Gly Ser Gln Arg Ser Ser Gly Arg Val Met Ile
110 115 120

cca ctg aag atg gag aca gaa gaa gat ggt acc atc tat gtg aac tca 495
Pro Leu Lys Met Glu Thr Glu Glu Asp Gly Thr Ile Tyr Val Asn Ser
125 130 135 140

aag cag tac cat gga att atc agg cga cgc cag tcc cga gca aag gct 543
 Lys Gln Tyr His Gly Ile Ile Arg Arg Arg Gln Ser Arg Ala Lys Ala
 145 150 155
 gaa aaa ctg agt aga tgc cgt aag cca tat atg cat cac tca cgc cat 591
 Glu Lys Leu Ser Arg Cys Arg Lys Pro Tyr Met His His Ser Arg His
 160 165 170
 ctc cat gct atg cgc cgt cct aga gga tct ggc ggg cgt ttc ttg aac 639
 Leu His Ala Met Arg Arg Pro Arg Gly Ser Gly Gly Arg Phe Leu Asn
 175 180 185
 acc aag aca gct gat gcg gct aag cag tct aag cag agt aat tct cag 687
 Thr Lys Thr Ala Asp Ala Lys Gln Ser Lys Pro Ser Asn Ser Gln
 190 195 200
 agt tct gaa gtc ttt cat cgc gaa aat gag acc ata aac tca tgc agg 735
 Ser Ser Glu Val Phe His Pro Glu Asn Glu Thr Ile Asn Ser Ser Arg
 205 210 215 220
 gaa gca aat gag tca aat ctc tgc gat tct gca gtt aca agt atg gat 783
 Glu Ala Asn Glu Ser Asn Leu Ser Asp Ser Ala Val Thr Ser Met Asp
 225 230 235
 tac ttt cta agt tgc tgc gct tat tct cct ggt ggc atg gtc atg cct 831
 Tyr Phe Leu Ser Ser Ser Ala Tyr Ser Pro Gly Gly Met Val Met Pro
 240 245 250
 atc aag tgg aat gca gca gca atg gat att ggc tgc tgc aaa ctt aat 879
 Ile Lys Trp Asn Ala Ala Met Asp Ile Gly Cys Cys Lys Leu Asn
 255 260 265
 ata tgatcagcag ataggggaca agacatgatt ggtoaccagt ccttttgtct 932
 Ile
 tgtcccttat ctttcagcca aacggaaaga gaacttgtgt cttggaaaaa agacattgag 992
 tttccttggt ttataagatt ggtcctttta ccatccgttt ggctgtaaaac aggcaaatca 1052
 tctttggctc atgcttcac aagttcttat ctctgtctgt tttcttctac gcattctcat 1112
 aagatctctg aactagttaa taacatttcc tagcatcatg tttcaactag tgtgtgttgt 1172
 aagaaactct gccttatttc cagatgatgt attgtgtgta acgtgtttat gaaacaaacg 1232
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<212> PRT

<213> Arabidopsis thaliana

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<223> G1334

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 35 40 45
 Gly Val Val Asp Lys Gln Thr Ser Thr Thr Leu Phe Thr Phe Ser Pro
 50 55 60
 Gly Gly Glu Lys Ser Ser Arg Asp Val Pro Lys Pro His Val Ala Phe
 65 70 75 80
 Ala Met Gln Ser Ala Cys Phe Glu Phe Gly Phe Ala Gln Pro Met Met
 85 90 95
 Tyr Thr Lys His Pro His Val Glu Gln Tyr Tyr Gly Val Val Ser Ala
 100 105 110
 Tyr Gly Ser Gln Arg Ser Ser Gly Arg Val Met Ile Pro Leu Lys Met
 115 120 125
 Glu Thr Glu Glu Asp Gly Thr Ile Tyr Val Asn Ser Lys Gln Tyr His
 130 135 140
 Gly Ile Ile Arg Arg Arg Gln Ser Arg Ala Lys Ala Glu Lys Leu Ser
 145 150 155 160
 Arg Cys Arg Lys Pro Tyr Met His His Ser Arg His Leu His Ala Met
 165 170 175
 Arg Arg Pro Arg Gly Ser Gly Gly Arg Phe Leu Asn Thr Lys Thr Ala
 180 185 190
 Asp Ala Ala Lys Gln Ser Lys Pro Ser Asn Ser Gln Ser Ser Glu Val
 195 200 205
 Phe His Pro Glu Asn Glu Thr Ile Asn Ser Ser Arg Glu Ala Asn Glu
 210 215 220
 Ser Asn Leu Ser Asp Ser Ala Val Thr Ser Met Asp Tyr Phe Leu Ser
 225 230 235 240
 Ser Ser Ala Tyr Ser Pro Gly Gly Met Val Met Pro Ile Lys Trp Asn
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<212> DNA

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210 215 220	
gag aag aaa cgt agc tgt cgc cga cct ctc tca gat cac aat gca aga	780
Glu Lys Lys Arg Ser Cys Arg Arg Pro Leu Ser Asp His Asn Ala Arg	
225 230 235	
cgt cgc aag cca aat cct gga agg aca tat gat ggg aaa cca cag gtg	828
Arg Arg Lys Pro Asn Pro Gly Arg Thr Tyr Asp Gly Lys Pro Glu Val	
240 245 250 255	
gat ttt gta tgg aac aga ttt gca ctt atc cat cca aga agt gag gaa	876
Asp Phe Val Trp Asn Arg Phe Ala Leu Ile His Pro Arg Ser Glu Glu	
260 265 270	
aag ttt cta tgg ccc agt tca aag cct gta cca tca aga gtc tta atg	924
Lys Phe Leu Trp Pro Ser Ser Lys Pro Val Pro Ser Arg Val Leu Met	
275 280 285	
ccg cag cct gca aag acc gag att tcc aat aag ctg ttc acc gag cac	972
Pro Gln Pro Ala Lys Thr Glu Ile Ser Asn Lys Leu Phe Thr Glu His	
290 295 300	
agt aga ttt gga ttg ttg gac ccc aaa aca aaa tcc gca aga gcg gag	1020
Ser Arg Phe Gly Leu Leu Asp Pro Lys Thr Lys Ser Ala Arg Ala Glu	
305 310 315	
tta ttc agt aaa gaa aag gtc aca atc tct tca cac atg ggt gct tct	1068
Leu Phe Ser Lys Glu Lys Val Thr Ile Ser Ser His Met Gly Ala Ser	
320 325 330 335	
caa gat ctt gat ggt gct ctc tct ctt ctg tca aat tca aca aca tgg	1116
Gln Asp Leu Asp Gly Ala Leu Ser Leu Leu Ser Asn Ser Thr Thr Trp	
340 345 350	
gtt tct tcc tct gac caa cca aga cgt ttt acc ctt gat cac cat ccc	1164
Val Ser Ser Ser Asp Gln Pro Arg Arg Phe Thr Leu Asp His His Pro	
355 360 365	
tca agc aac ctc caa ccc gta gct aac cgg tct gcg gct caa ctc agt	1212
Ser Ser Asn Leu Gln Pro Val Ala Asn Arg Ser Ala Ala Gln Leu Ser	
370 375 380	
tca gtg tcc ggc tat tgg cag ccg gac cca ccc gca gtt gaa ggc ccg	1260
Ser Val Ser Gly Tyr Trp Gln Pro Asp Pro Pro Ala Val Glu Gly Pro	
385 390 395	
acc gct ctg cat aga aat ggg gca ggc cag ttt aat gaa aac tac ttc	1308
Thr Ala Leu His Arg Asn Gly Ala Gly Gln Phe Asn Glu Asn Tyr Phe	
400 405 410 415	
agc ttg aac cag ttt tat aac tgaaagctgt atgcctttaa atcctattta	1359
Ser Leu Asn Gln Phe Tyr Asn	
420	
ggatcaagca agctagtgat aagttaagat aggagctgtg aaacttgcaa gacaccaa	1419

cctctcttat ttctttgtcc aaatattttc atgggttaga gagctttgac aattgtcttt 1479
 aatatcaact ttatcgtgtt atacattagg attataaaaa aaaaaaaaaa a 1530

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 <213> *Arabidopsis thaliana*

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 <223> G718

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 20 25 30
 Met Glu Trp Glu Ile Asp Gly Phe Asp Cys Thr Ser Leu Tyr Ser Ser
 35 40 45
 Ser Phe Ala Tyr Ala Gly Ser Ser Gly Ser Asp Ile Ala His Ala Phe
 50 55 60
 Ser Lys Ser Ser Lys Ser Thr Ser Ile Ser Ser Ser Ala Glu Val
 65 70 75 80
 Arg Thr His Asn Phe Thr Ser Glu Thr Gly Glu Ser Leu Pro Gly Glu
 85 90 95
 Phe Ala Lys Gly Ile Asp Thr Ser Pro Thr Leu Glu Leu Ser Phe Gly
 100 105 110
 Ser Gly Asp Pro Val Leu Gly Leu Lys Leu Ala Lys Arg Thr Tyr Phe
 115 120 125
 Glu Asp Phe Trp Glu Val Glu Asn Ala Lys Gly Leu Gly Leu Pro Val
 130 135 140
 Thr Leu Ala Ser Ser Ser Val Ser Pro Val Lys Lys Ser Lys Ser Ile
 145 150 155 160
 Pro Gln Thr Leu Gln Thr Pro His Cys Gln Val Glu Gly Cys Asn Leu
 165 170 175
 Asp Leu Ser Ser Ala Lys Asp Tyr His Arg Lys His Arg Ile Cys Glu
 180 185 190
 Asn His Ser Lys Phe Pro Lys Val Val Val Ser Gly Val Glu Arg Arg
 195 200 205
 Phe Cys Gln Gln Cys Ser Arg Phe His Cys Leu Ser Glu Phe Asp Glu
 210 215 220

Lys Lys Arg Ser Cys Arg Arg Pro Leu Ser Asp His Asn Ala Arg Arg
225 230 235 240

Arg Lys Pro Asn Pro Gly Arg Thr Tyr Asp Gly Lys Pro Gln Val Asp
245 250 255

Phe Val Trp Asn Arg Phe Ala Leu Ile His Pro Arg Ser Glu Glu Lys
260 265 270

Phe Leu Trp Pro Ser Ser Lys Pro Val Pro Ser Arg Val Leu Met Pro
275 280 285

Gln Pro Ala Lys Thr Glu Ile Ser Asn Lys Leu Phe Thr Glu His Ser
290 295 300

Arg Phe Gly Leu Leu Asp Pro Lys Thr Lys Ser Ala Arg Ala Glu Leu
305 310 315 320

Phe Ser Lys Glu Lys Val Thr Ile Ser Ser His Met Gly Ala Ser Gln
325 330 335

Asp Leu Asp Gly Ala Leu Ser Leu Leu Ser Asn Ser Thr Thr Trp Val
340 345 350

Ser Ser Ser Asp Gln Pro Arg Arg Phe Thr Leu Asp His His Pro Ser
355 360 365

Ser Asn Leu Gln Pro Val Ala Asn Arg Ser Ala Ala Gln Leu Ser Ser
370 375 380

Val Ser Gly Tyr Trp Gln Pro Asp Pro Pro Ala Val Glu Gly Pro Thr
385 390 395 400

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405 410 415

Leu Asn Gln Phe Tyr Asn
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<210> 133

<211> 885

<212> DNA

<213> Arabidopsis thaliana

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<222> (25)..(780)

<223> G763

<400> 133

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Gly Val Leu Arg Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu
10 15 20 25

gaa ctt gtg gtt caa tac ctt aag agg aaa gtt tgt tct tct cct ttg 147
 Glu Leu Val Val Gln Tyr Leu Lys Arg Lys Val Cys Ser Ser Pro Leu
 30 35 40

cca gct tca atc atc cct gag ttt gat gtt tgc aga gct gat cct tgg 195
 Pro Ala Ser Ile Ile Pro Glu Phe Asp Val Cys Arg Ala Asp Pro Trp
 45 50 55

gat tta cct cgc aat ttg gag aaa gag agg tac ttc ttt agc aca agg 243
 Asp Leu Pro Arg Asn Leu Glu Lys Glu Arg Tyr Phe Ser Thr Arg
 60 65 70

gaa gct aaa tac cca aat ggg aac cgg tct aac cgg gca act ggg tct 291
 Glu Ala Lys Tyr Pro Asn Gly Asn Arg Ser Asn Arg Ala Thr Gly Ser
 75 80 85

ggt tat tgg aaa gct acc ggt att gat aaa cgg gtt gtg acc tct aga 339
 Gly Tyr Trp Lys Ala Thr Gly Ile Asp Lys Arg Val Val Thr Ser Arg
 90 95 100 105

gga aat caa atc gtt ggt ttg aag aaa act ctt gtc ttc tac aaa ggc 387
 Gly Asn Gln Ile Val Gly Leu Lys Lys Thr Leu Val Phe Tyr Lys Gly
 110 115 120

aaa cca cct cat ggc tca aga acc gat tgg atc atg cac gaa tat cgc 435
 Lys Pro Pro His Gly Ser Arg Thr Asp Trp Ile Met His Glu Tyr Arg
 125 130 135

ctc tct tct tct cct cgg agt tct atg ggt ccc act cag aac tgg gta 483
 Leu Ser Ser Ser Pro Pro Ser Ser Met Gly Pro Thr Gln Asn Trp Val
 140 145 150

ctc tgt cgt atc ttc ttg aag aaa aga gcc ggt aac aag aac gac gac 531
 Leu Cys Arg Ile Phe Leu Lys Lys Arg Ala Gly Asn Lys Asn Asp Asp
 155 160 165

gac gac gga gat agc cgt aat ctt aga cat aat aat aat aac aat tcg 579
 Asp Asp Gly Asp Ser Arg Asn Leu Arg His Asn Asn Asn Asn Ser
 170 175 180 185

agt gac caa att gag ata att aca aca gac caa aca gat gat aaa aca 627
 Ser Asp Gln Ile Glu Ile Ile Thr Thr Asp Gln Thr Asp Lys Thr
 190 195 200

aaa cca atc ttc ttt gat ttc atg aga aaa gaa aga aca aca gat ttg 675
 Lys Pro Ile Phe Phe Asp Phe Met Arg Lys Glu Arg Thr Thr Asp Leu
 205 210 215

aac ctt ttg cgg agc tct oct tct tcc gat cat gct tca agt gga gtc 723
 Asn Leu Leu Pro Ser Ser Pro Ser Ser Asp His Ala Ser Ser Gly Val
 220 225 230

acg acg gag atc ttc tct tct tcc gat gaa gag acc agt agt tgc aat 771
 Thr Thr Glu Ile Phe Ser Ser Ser Asp Glu Glu Thr Ser Ser Cys Asn
 235 240 245

Met Arg Lys Glu Arg Thr Thr Asp Leu Asn Leu Pro Ser Ser Pro
210 215 220

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225 230 235 240

Ser Asp Glu Glu Thr Ser Ser Cys Asn Ser Phe Arg
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<222> (22)..(612)

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Thr Glu Leu Arg Leu Gly Leu Pro Gly Arg Asp Val Ala Glu Lys Met
                        15 20 25

atg aag aag aga gct ttc acg gag atg aat atg acg tcg tcg ggt agt 147
Met Lys Lys Arg Ala Phe Thr Glu Met Asn Met Thr Ser Ser Gly Ser
                        30 35 40

aat agt gat caa tgt gaa agc ggc gtc gtt tca tct ggt ggt gac gct 195
Asn Ser Asp Gln Cys Glu Ser Gly Val Val Ser Ser Gly Gly Asp Ala
                        45 50 55

gag aag gtt aat gat tcg ccg gcg gcg aaa agc cag gtg gtg ggg tgg 243
Glu Lys Val Asn Asp Ser Pro Ala Ala Lys Ser Gln Val Val Gly Trp
                        60 65 70

cca ccg gtt tgt tct tac ccg aag aaa aac agc tgt aag gaa gct tcg 291
Pro Pro Val Cys Ser Tyr Arg Lys Lys Asn Ser Cys Lys Glu Ala Ser
                        75 80 85 90

acc acg aaa gtg ggg tta ggg tat gtg aaa gtg agc atg gat ggt gtg 339
Thr Thr Lys Val Gly Leu Gly Tyr Val Lys Val Ser Met Asp Gly Val
                        95 100 105

cct tat ttg agg aag atg gat ctt ggt tcg agc caa ggc tat gat gat 387
Pro Tyr Leu Arg Lys Met Asp Leu Gly Ser Ser Gln Gly Tyr Asp Asp
                        110 115 120

cta gcc ttt gct ctt gat aag ctc ttc ggt ttc cgt gcc atc ggt gtg 435
Leu Ala Phe Ala Leu Asp Lys Leu Phe Gly Phe Arg Gly Ile Gly Val
                        125 130 135

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gcc ttg aaa gat ggt gac aac tgc gaa tac gtt acc ata tac gaa gac 483
 Ala Leu Lys Asp Gly Asp Asn Cys Glu Tyr Val Thr Ile Tyr Glu Asp
 140 145 150

aaa gat gga gac tgg atg ctc gcc ggt gat gta cct tgg ggg atg ttt 531
 Lys Asp Gly Asp Trp Met Leu Ala Gly Asp Val Pro Trp Gly Met Phe
 155 160 165 170

cta gag tca tgc aag agg ttg aga ata atg aaa aga tgc gat gct acc 579
 Leu Glu Ser Cys Lys Arg Leu Arg Ile Met Lys Arg Ser Asp Ala Thr
 175 180 185

ggg ttt ggg ctg cag cct aga gga gta gac gag tgatgatgac ttgaacaaga 632
 Gly Phe Gly Leu Gln Pro Arg Gly Val Asp Glu
 190 195

agcaaggagc tggttcatta atttaactctt aaacttgatc atcaagatcc tttagaacat 692
 ttttcctatt catgttatat aaatatatat gttatagtat attattttgc aacaaaaattt 752
 catgttaaaaa aaaaaaaaaa aaaaaaa 779

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 <213> Arabidopsis thaliana

<220>
 <223> G462

<400> 136
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 Thr Glu Met Asn Met Thr Ser Ser Gly Ser Asn Ser Asp Gln Cys Glu
 35 40 45
 Ser Gly Val Val Ser Ser Gly Gly Asp Ala Glu Lys Val Asn Asp Ser
 50 55 60
 Pro Ala Ala Lys Ser Gln Val Val Gly Trp Pro Pro Val Cys Ser Tyr
 65 70 75 80
 Arg Lys Lys Asn Ser Cys Lys Glu Ala Ser Thr Thr Lys Val Gly Leu
 85 90 95
 Gly Tyr Val Lys Val Ser Met Asp Gly Val Pro Tyr Leu Arg Lys Met
 100 105 110
 Asp Leu Gly Ser Ser Gln Gly Tyr Asp Asp Leu Ala Phe Ala Leu Asp
 115 120 125
 Lys Leu Phe Gly Phe Arg Gly Ile Gly Val Ala Leu Lys Asp Gly Asp
 130 135 140

Asn Cys Glu Tyr Val Thr Ile Tyr Glu Asp Lys Asp Gly Asp Trp Met
145 150 155 160

Leu Ala Gly Asp Val Pro Trp Gly Met Phe Leu Glu Ser Cys Lys Arg
165 170 175

Leu Arg Ile Met Lys Arg Ser Asp Ala Thr Gly Phe Gly Leu Gln Pro
180 185 190

Arg Gly Val Asp Glu
195

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<222> (186)..(1037)

<223> G782

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tcaatttgat cgtctctgaat tcctcgtcct atttaggggt tcgatcacaa tctgaagagg 180

aggtc atg gac gtt tct gct aga aag tca caa aaa gct ggg cgc gaa aag 230

Met Asp Val Ser Ala Arg Lys Ser Gln Lys Ala Gly Arg Glu Lys
1 5 10 15

ttg agg agg gaa aaa ctg aat gag cat ttt gtt gaa ctg gga aat gta 278

Leu Arg Arg Glu Lys Leu Asn Glu His Phe Val Glu Leu Gly Asn Val
20 25 30

ctc gat cca gag aga ccc aag aat gac aaa gcc acg att ctg act gat 326

Leu Asp Pro Glu Arg Pro Lys Asn Asp Lys Ala Thr Ile Leu Thr Asp
35 40 45

act gtt cag ttg ttg aaa gag ctc aca tct gaa gtc aac aaa ctg aaa 374

Thr Val Gln Leu Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys
50 55 60

tct gag tac acc gca ttg aca gat gag tcc cgc gag ttg aca cag gag 422

Ser Glu Tyr Thr Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu
65 70 75

aaa aac gac ctg aga gaa gaa aag aca tcg ctg aaa tca gat ata gag 470

Lys Asn Asp Leu Arg Glu Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu
80 85 90 95

aat ctc aat ctt caa tac cag cag aga tta agg tca atg tct cca tgg 518

Asn Leu Asn Leu Gln Tyr Gln Gln Arg Leu Arg Ser Met Ser Pro Trp
100 105 110

gga gct gcg atg gat cac aca gtc atg atg gct cca cca ccc tcc ttt 566
 Gly Ala Ala Met Asp His Thr Val Met Met Ala Pro Pro Ser Phe
 115 120 125

cca tac cct atg cct att gct atg cct ccc ggg tca atc cca atg cat 614
 Pro Tyr Pro Met Pro Ile Ala Met Pro Pro Gly Ser Ile Pro Met His
 130 135 140

cca tca atg cca tct tac aca tac ttt ggg aac cag aac cct agc atg 662
 Pro Ser Met Pro Ser Tyr Thr Tyr Phe Gly Asn Gln Asn Pro Ser Met
 145 150 155

atc cca gct cca tgt cct aca tac atg ccc tac atg cct cct aat aca 710
 Ile Pro Ala Pro Cys Pro Thr Tyr Met Pro Tyr Met Pro Pro Asn Thr
 160 165 170 175

gtc gtt gag caa caa tcc gtg cac att cca cag aac ccc ggt aac cgt 758
 Val Val Glu Gln Gln Ser Val His Ile Pro Gln Asn Pro Gly Asn Arg
 180 185 190

tct cgg gaa cct aga gca aag gtt tca aga gag agc aga tct gag aaa 806
 Ser Arg Glu Pro Arg Ala Lys Val Ser Arg Glu Ser Arg Ser Glu Lys
 195 200 205

gca gag gac tcc aac gaa gtt gca aca caa ctc gaa tta aaa acc cct 854
 Ala Glu Asp Ser Asn Glu Val Ala Thr Gln Leu Glu Leu Lys Thr Pro
 210 215 220

gga tct act tct gat aag gat aca ttg caa agg cca gag aag aca aag 902
 Gly Ser Thr Ser Asp Lys Asp Thr Leu Gln Arg Pro Glu Lys Thr Lys
 225 230 235

aga tgt aag aga aac aac aac aac aac tca ata gaa gaa agc tct cat 950
 Arg Cys Lys Arg Asn Asn Asn Asn Asn Ser Ile Glu Glu Ser Ser His
 240 245 250 255

tct agc aag tgt tca tct tct ccg agc gta cga gac cac agt tct tcc 998
 Ser Ser Lys Cys Ser Ser Ser Pro Ser Val Arg Asp His Ser Ser Ser
 260 265 270

agt agc gta gct ggt gcc caa aaa cct gat gat gca aaa tgattcgaaa 1047
 Ser Ser Val Ala Gly Gly Gln Lys Pro Asp Asp Ala Lys
 275 280

gaatctgatg ttgatcatct caagtatcca agtatcgttt cgatgagtac tgtatatagt 1107

gcgagtacaa aatgcactta gctgtttaaa gcagtggttt gatgcaccgt ggcatcgtt 1167

ttctctggat agtcatttct cagatgattt tcatccttaa taggtctgct ttagttctaa 1227

aactcgatg atttgtaatt tccagtgtcc aaatctacta attttattaa aaaaa 1282

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<211> 284

<212> PRT

<213> Arabidopsis thaliana

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<223> G782

<400> 138

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Asp Pro Glu Arg Pro Lys Asn Asp Lys Ala Thr Ile Leu Thr Asp Thr
          35              40              45

Val Gln Leu Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys Ser
          50              55              60

Glu Tyr Thr Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu Lys
          65              70              75              80

Asn Asp Leu Arg Glu Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu Asn
          85              90              95

Leu Asn Leu Gln Tyr Gln Gln Arg Leu Arg Ser Met Ser Pro Trp Gly
          100              105              110

Ala Ala Met Asp His Thr Val Met Met Ala Pro Pro Pro Ser Phe Pro
          115              120              125

Tyr Pro Met Pro Ile Ala Met Pro Pro Gly Ser Ile Pro Met His Pro
          130              135              140

Ser Met Pro Ser Tyr Thr Tyr Phe Gly Asn Gln Asn Pro Ser Met Ile
          145              150              155              160

Pro Ala Pro Cys Pro Thr Tyr Met Pro Tyr Met Pro Pro Asn Thr Val
          165              170              175

Val Glu Gln Gln Ser Val His Ile Pro Gln Asn Pro Gly Asn Arg Ser
          180              185              190

Arg Glu Pro Arg Ala Lys Val Ser Arg Glu Ser Arg Ser Glu Lys Ala
          195              200              205

Glu Asp Ser Asn Glu Val Ala Thr Gln Leu Glu Leu Lys Thr Pro Gly
          210              215              220

Ser Thr Ser Asp Lys Asp Thr Leu Gln Arg Pro Glu Lys Thr Lys Arg
          225              230              235              240

Cys Lys Arg Asn Asn Asn Asn Ser Ile Glu Glu Ser Ser His Ser
          245              250              255

Ser Lys Cys Ser Ser Ser Pro Ser Val Arg Asp His Ser Ser Ser
          260              265              270

Ser Val Ala Gly Gly Gln Lys Pro Asp Asp Ala Lys
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 <223> G783

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gttctgtaat aaaagcaaag atg gta tcg aaa act cct tct aca tcg tct gat 113
 Met Val Ser Lys Thr Pro Ser Thr Ser Ser Asp
 1 5 10

gaa gca aat gct act gca gat gaa aga tgt aga aaa ggt aaa gta ccg 161
 Glu Ala Asn Ala Thr Ala Asp Glu Arg Cys Arg Lys Gly Lys Val Pro
 15 20 25

aaa agg atc aac aag gcc gtt cgt gag agg ctt aag cgt gag cat ttg 209
 Lys Arg Ile Asn Lys Ala Val Arg Glu Arg Leu Lys Arg Glu His Leu
 30 35 40

aat gag ctt ttc att gaa tta gcc gat act ctt gaa ctg aat caa cag 257
 Asn Glu Leu Phe Ile Glu Leu Ala Asp Thr Leu Glu Leu Asn Gln Gln
 45 50 55

aac agt ggg aaa gct tct ata cta tgc gaa gct act cga ttc ttg aag 305
 Asn Ser Gly Lys Ala Ser Ile Leu Cys Glu Ala Thr Arg Phe Leu Lys
 60 65 70 75

gac gtg ttt ggt caa att gag tct ctt aga aag gag cat gct tct ctc 353
 Asp Val Phe Gly Gln Ile Glu Ser Leu Arg Lys Glu His Ala Ser Leu
 80 85 90

cta tct gaa tct agc tat gta acc aca gag aag aat gag ctc aag gaa 401
 Leu Ser Glu Ser Ser Tyr Val Thr Thr Glu Lys Asn Glu Leu Lys Glu
 95 100 105

gaa aca tca gtg ctt gag act gag att tcg aaa cta caa aac gag att 449
 Glu Thr Ser Val Leu Glu Thr Glu Ile Ser Lys Leu Gln Asn Glu Ile
 110 115 120

gaa gct aga gcg aat cag tcg aaa cct gac ttg aac acc tct cct gca 497
 Glu Ala Arg Ala Asn Gln Ser Lys Pro Asp Leu Asn Thr Ser Pro Ala
 125 130 135

ccc gag tac cat cat cat tat caa caa caa cat cct gaa cgt gta 545
 Pro Glu Tyr His His His Tyr Gln Gln Gln His Pro Glu Arg Val
 140 145 150 155

tct cag ttc cca gga ctt ccc att ttc caa ggc ccc ggc ttt caa caa 593
 Ser Gln Phe Pro Gly Leu Pro Ile Phe Gln Gly Pro Gly Phe Gln Gln
 160 165 170

tct gct aca act ctt cat cct cct gca aca gtt ctt gtc ctt cca ata 641
 Ser Ala Thr Thr Leu His Pro Pro Ala Thr Val Leu Val Leu Pro Ile
 175 180 185

caa cct gat ccc cag aca caa gat atc tca gaa atg act caa gcg cag 689
 Gln Pro Asp Pro Gln Thr Gln Asp Ile Ser Glu Met Thr Gln Ala Gln
 190 195 200

cag cct ttg atg ttt aat agc tca aat gtg agt aac cca tgt cca agg 737
 Gln Pro Leu Met Phe Asn Ser Ser Asn Val Ser Asn Pro Cys Pro Arg
 205 210 215

tat gct agc gcg gct gac tcg tgg tct tct cgg cta ctt gga gag cgg 785
 Tyr Ala Ser Ala Ala Asp Ser Trp Ser Ser Arg Leu Leu Gly Glu Arg
 220 225 230 235

ctg aaa gcc agt gaa tgaggtcttg aacggctcca catggagtag caacgcaagt 840
 Leu Lys Ala Ser Glu
 240

tataagacat ggcaacttat gaaggactct ggttttgtat tttttaatac atcgttctga 900

tgctccttgtg ggtttggcct tggctatttc ttgtttttga tggttgttca taggatcagg 960

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 aaaaaaaaaa 1027

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 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G783

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Ala Val Arg Glu Arg Leu Lys Arg Glu His Leu Asn Glu Leu Phe Ile
 35 40 45

Glu Leu Ala Asp Thr Leu Glu Leu Asn Gln Gln Asn Ser Gly Lys Ala
 50 55 60

Ser Ile Leu Cys Glu Ala Thr Arg Phe Leu Lys Asp Val Phe Gly Gln
 65 70 75 80

Ile Glu Ser Leu Arg Lys Glu His Ala Ser Leu Leu Ser Glu Ser Ser
 85 90 95

Tyr Val Thr Thr Glu Lys Asn Glu Leu Lys Glu Glu Thr Ser Val Leu
100 105 110

Glu Thr Glu Ile Ser Lys Leu Gln Asn Glu Ile Glu Ala Arg Ala Asn
115 120 125

Gln Ser Lys Pro Asp Leu Asn Thr Ser Pro Ala Pro Glu Tyr His His
130 135 140

His His Tyr Gln Gln Gln His Pro Glu Arg Val Ser Gln Phe Pro Gly
145 150 155 160

Leu Pro Ile Phe Gln Gly Pro Gly Phe Gln Gln Ser Ala Thr Thr Leu
165 170 175

His Pro Pro Ala Thr Val Leu Val Leu Pro Ile Gln Pro Asp Pro Gln
180 185 190

Thr Gln Asp Ile Ser Glu Met Thr Gln Ala Gln Gln Pro Leu Met Phe
195 200 205

Asn Ser Ser Asn Val Ser Asn Pro Cys Pro Arg Tyr Ala Ser Ala Ala
210 215 220

Asp Ser Trp Ser Ser Arg Leu Leu Gly Glu Arg Leu Lys Ala Ser Glu
225 230 235 240

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<212> DNA

<213> Arabidopsis thaliana

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<222> (433) ..(1185)

<223> G786

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ctacttttga tttcgaaaaa atttactgtg agttgtttaa gagtctggta ttctgaagag 180

ctgtctgtgg gggagcttct ggtttggggg gtaagggctc tgggtgaaac tcgtgatatc 240

tttagtatga tggccataac ttgatatagc atttggttcc gtgtgtcaac ttagttagt 300

agtaactgag cagctggaag cttacaaagg cgacaaatcg gtagtagama atattcaagc 360

agcttgtagt ttgaggtgta caacttggtt ttctctttgc gtttcccttt ttacgtttgc 420

acgggttttc tg agt cag aac aat cag ttt cct cac ttc tca gat gaa gtg 471

Met Gln Asn Asn Gln Phe Pro His Phe Ser Asp Glu Val
1 5 10

ggg gac aga aat atg cac aac ccg tat gca tca ggg tca tcc tat gat	519
Gly Asp Arg Asn Met His Asn Pro Tyr Ala Ser Gly Ser Ser Tyr Asp	
15 20 25	
gct ttg ttc cca cca tgt gca aag ttg cca tac cat ggt gtt gaa ctt	567
Ala Leu Phe Pro Pro Cys Ala Lys Leu Pro Tyr His Gly Val Glu Leu	
30 35 40 45	
caa ccg tct gcg gtc tgt cca aag aac ttt gtc atc ttc gat caa aca	615
Gln Pro Ser Ala Val Cys Pro Lys Asn Phe Val Ile Phe Asp Gln Thr	
50 55 60	
tat gac cgc agc caa gtg atg tac cat cct gag ctg act cat aag ctc	663
Tyr Asp Arg Ser Gln Val Met Tyr His Pro Glu Leu Thr His Lys Leu	
65 70 75	
atg aat acc cct tcg ttg aac aat tta gct tcg acg ttt cag aac gag	711
Met Asn Thr Pro Ser Leu Asn Asn Leu Ala Ser Thr Phe Gln Asn Glu	
80 85 90	
tat gtt ggg gga agt tat ggt aac tat ggt aac tat gag caa gaa gta	759
Tyr Val Gly Gly Ser Tyr Gly Asn Tyr Gly Asn Tyr Glu Gln Glu Val	
95 100 105	
tcc tct tct tat caa gaa gat cca aat gag atc gat gct ctc ttg agc	807
Ser Ser Ser Tyr Gln Glu Asp Pro Asn Glu Ile Asp Ala Leu Leu Ser	
110 115 120 125	
gca gat gaa gat tat gaa gag aat gat gat aat gaa ggt gaa gag gat	855
Ala Asp Glu Asp Tyr Glu Glu Asn Asp Asp Asn Glu Gly Glu Glu Asp	
130 135 140	
ggg ggt gat tca gaa gaa gtc agc act gct cgt act tct tcc agg gat	903
Gly Gly Asp Ser Glu Glu Val Ser Thr Ala Arg Thr Ser Ser Arg Asp	
145 150 155	
tat gga aac acc aca gca gaa tct tgt tgt tcc agt tat ggt tac aac	951
Tyr Gly Asn Thr Thr Ala Glu Ser Cys Cys Ser Ser Tyr Gly Tyr Asn	
160 165 170	
aac aac aac aac aac aac tca agg aag cag agt tta tcg ggc agt gct	999
Asn Asn Asn Asn Asn Asn Ser Arg Lys Gln Ser Leu Ser Gly Ser Ala	
175 180 185	
agt agt agt aac aat gat ggg aaa gga cgt aaa aag atg aag aag atg	1047
Ser Ser Ser Asn Asn Asp Gly Lys Gly Arg Lys Lys Met Lys Lys Met	
190 195 200 205	
atg gga gta ttg agg aga att gtc cct gga gga gaa cag atg aat aca	1095
Met Gly Val Leu Arg Arg Ile Val Pro Gly Gly Glu Gln Met Asn Thr	
210 215 220	
gct tgc gtt ctt gat gaa gct gtt cag tat ctc aag tca ctt aaa atc	1143
Ala Cys Val Leu Asp Glu Ala Val Gln Tyr Leu Lys Ser Leu Lys Ile	
225 230 235	

Asn Asn Asn Ser Arg Lys Gln Ser Leu Ser Gly Ser Ala Ser Ser Ser
180 185 190

Asn Asn Asp Gly Lys Gly Arg Lys Lys Met Lys Lys Met Met Gly Val
195 200 205

Leu Arg Arg Ile Val Pro Gly Gly Glu Gln Met Asn Thr Ala Cys Val
210 215 220

Leu Asp Glu Ala Val Gln Tyr Leu Lys Ser Leu Lys Ile Glu Ala Gln
225 230 235 240

Lys Leu Gly Val Gly His Phe Ser Asn Gln Ser
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<213> Arabidopsis thaliana

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<222> (138)..(1043)

<223> G793

<400> 143

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ctttactcgt ttccttc atg gct aat aac aac aac atc cca cat gat agc 170
Met Ala Asn Asn Asn Asn Ile Pro His Asp Ser
1 5 10

atc tcc gat cca tct cct acc gac gat ttc ttc gag cag atc ctc ggg 218
Ile Ser Asp Pro Ser Pro Thr Asp Asp Phe Phe Glu Gln Ile Leu Gly
15 20 25

ctt tcc aac ttc tcc ggt tct tca ggt tct ggt ctc tct gga atc ggc 266
Leu Ser Asn Phe Ser Gly Ser Ser Gly Ser Gly Leu Ser Gly Ile Gly
30 35 40

ggc gtg ggt cca cct ccg atg atg ctt cag ctt ggt tca ggc aac gaa 314
Gly Val Gly Pro Pro Pro Met Met Leu Gln Leu Gly Ser Gly Asn Glu
45 50 55

ggg aat cat aat cat atg ggt gcc att gga gga ggt gga cct gta ggg 362
Gly Asn His Asn His Met Gly Ala Ile Gly Gly Gly Gly Pro Val Gly
60 65 70 75

ttt cat aat cag atg ttt ccg ttg gga tta agt ctc gat caa ggg aaa 410
Phe His Asn Gln Met Phe Pro Leu Gly Leu Ser Leu Asp Gln Gly Lys
80 85 90

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 agaagaaaa agctctcgct tgcttggtta gtatttatca ttttgatgaa agtaactctt 1263
 ttttgttcaa agacttttagt gtgattttca ggaccaagggt ctttgagggt agtgctagct 1323
 gtagtaatag taatgaaggt gtggatcgt gtttttgaat tatgtaaaaa aggaacaaaa 1383
 aacaaatgtt ggtattatat tatggttttg cctgaaa 1420

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 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G793

<400> 144
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 20 25 30
 Gly Ser Ser Gly Ser Gly Leu Ser Gly Ile Gly Gly Val Gly Pro Pro
 35 40 45
 Pro Met Met Leu Gln Leu Gly Ser Gly Asn Glu Gly Asn His Asn His
 50 55 60
 Met Gly Ala Ile Gly Gly Gly Gly Pro Val Gly Phe His Asn Gln Met
 65 70 75 80
 Phe Pro Leu Gly Leu Ser Leu Asp Gln Gly Lys Gly His Gly Phe Leu
 85 90 95
 Lys Pro Asp Glu Thr Gly Lys Arg Phe Gln Asp Asp Val Leu Asp Asn
 100 105 110
 Arg Cys Ser Ser Met Lys Pro Ile Phe His Gly Gln Pro Met Ser Gln
 115 120 125
 Pro Ala Pro Pro Met Pro His Gln Gln Ser Thr Ile Arg Pro Arg Val
 130 135 140
 Arg Ala Arg Arg Gly Gln Ala Thr Asp Pro His Ser Ile Ala Glu Arg
 145 150 155 160
 Leu Arg Arg Glu Arg Ile Ala Glu Arg Ile Arg Ser Leu Gln Glu Leu
 165 170 175
 Val Pro Thr Val Asn Lys Thr Asp Arg Ala Ala Met Ile Asp Glu Ile
 180 185 190
 Val Asp Tyr Val Lys Phe Leu Arg Leu Gln Val Lys Val Leu Ser Met
 195 200 205

Ser Arg Leu Gly Gly Ala Gly Ala Val Ala Pro Leu Val Thr Glu Met
 210 215 220

Pro Leu Ser Ser Ser Val Glu Asp Glu Thr Gln Ala Val Trp Glu Lys
 225 230 235 240

Trp Ser Asn Asp Gly Thr Glu Arg Gln Val Ala Lys Leu Met Glu Glu
 245 250 255

Asn Val Gly Ala Ala Met Gln Leu Leu Gln Ser Lys Ala Leu Cys Ile
 260 265 270

Met Pro Ile Ser Leu Ala Met Ala Ile Tyr His Ser Gln Pro Pro Asp
 275 280 285

Thr Ser Ser Ser Ile Val Lys Pro Glu Met Asn Pro Pro Pro
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<211> 1009

<212> DNA

<213> Arabidopsis thaliana

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<222> (27)..(743)

<223> G801

<400> 145

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 1 5

aac gcc atc ata gtc gag cag acg tca aac aaa gga cct ctt aac gcc 101
 Asn Gly Ile Ile Val Glu Gln Thr Ser Asn Lys Gly Pro Leu Asn Ala
 10 15 20 25

gtt aag aaa cca ccg tct aaa gat cga cac agc aaa gtt gac gga aga 149
 Val Lys Lys Pro Pro Ser Lys Asp Arg His Ser Lys Val Asp Gly Arg
 30 35 40

gga aga agg att cgt atg cca atc att tgc gca gct cga gtt ttt caa 197
 Gly Arg Arg Ile Arg Met Pro Ile Ile Cys Ala Ala Arg Val Phe Gln
 45 50 55

ttg acc aga gag tta ggt cac aag tcc gat ggt caa acc ata gag tgg 245
 Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Gln Thr Ile Glu Trp
 60 65 70

ctt ctc cgt caa gct gag cct tct atc ata gcc gcc act gga act gcc 293
 Leu Leu Arg Gln Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly Thr Gly
 75 80 85

act act ccg gcg agt ttc tcc act gct tct ctc tcc act tct tct ccg 341
 Thr Thr Pro Ala Ser Phe Ser Thr Ala Ser Leu Ser Thr Ser Ser Pro
 90 95 100 105

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ttt act ctc ggg aaa cgt gtc gtc aga gcg gag gaa gga gaa tcc ggc 389
Phe Thr Leu Gly Lys Arg Val Val Arg Ala Glu Glu Gly Glu Ser Gly
110 115 120

ggc gga gga gga gga ggg tta aca gtg gga cac aca atg ggg act tcg 437
Gly Gly Gly Gly Gly Gly Leu Thr Val Gly His Thr Met Gly Thr Ser
125 130 135

tta atg ggt ggt ggt ggt tct ggt ggg ttt tgg gct gtt cgg gcg agg 485
Leu Met Gly Gly Gly Gly Ser Gly Gly Phe Trp Ala Val Pro Ala Arg
140 145 150

ccg gat ttc gga caa gtc tgg agc ttt gca acc gga gct cca ccg gaa 533
Pro Asp Phe Gly Gln Val Trp Ser Phe Ala Thr Gly Ala Pro Pro Glu
155 160 165

atg gtt ttt gcg cag cag cag caa cca gct aca ctc ttc gtc cgc cac 581
Met Val Phe Ala Gln Gln Gln Gln Pro Ala Thr Leu Phe Val Arg His
170 175 180 185

cag cag caa cag caa gct tcc gcc gcc gca gca gct gca atg ggt gag 629
Gln Gln Gln Gln Gln Ala Ser Ala Ala Ala Ala Ala Met Gly Glu
190 195 200

gct tca gca gct aga gtt ggg aat tat ctt ccg ggt cat cat ctc aat 677
Ala Ser Ala Ala Arg Val Gly Asn Tyr Leu Pro Gly His His Leu Asn
205 210 215

ttg ctt gct tct ttg tct ggt gga gct aac ggg tcg ggt cgg agg gaa 725
Leu Leu Ala Ser Leu Ser Gly Gly Ala Asn Gly Ser Gly Arg Arg Glu
220 225 230

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Asp Asp His Glu Pro Arg
235

atagaaaaat tcttatgttt tatgtcatcg aaagtgttta gaaagtacct ctaatttcgc 833

gtttcttttg ctcttttttt acttaattta agcttattgc ttgtttgatt agggtttttag 893

ggtttaagaa tatttgggtct cgtaaatttg ttccggagag tgatagaaag agagagagat 953

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Met Asp Leu Ser Asp Ile Arg Asn Asn Asn	
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aac gac acc gcc gcc gtc gcc acc gga gga gga gca aga cag cta gtt	220
Asn Asp Thr Ala Ala Val Ala Thr Gly Gly Gly Ala Arg Gln Leu Val	
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Asp Ala Ser Leu Ser Ile Val Pro Arg Ser Thr Pro Pro Glu Asp Ser	
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Thr Leu Ala Thr Thr Ser Ser Thr Ala Thr Thr Thr Thr Lys Arg	
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Ser Thr Lys Asp Arg His Thr Lys Val Asp Gly Arg Gly Arg Arg Ile	
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Arg Met Pro Ala Leu Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu	
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Leu Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu Leu Gln Gln	
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gct gag cca gct att gtt gct gct aca ggt aca gga act att ccg gcg	508
Ala Glu Pro Ala Ile Val Ala Ala Thr Gly Thr Gly Thr Ile Pro Ala	
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Asn Phe Ser Thr Leu Ser Val Ser Leu Arg Ser Ser Gly Ser Thr Leu	
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Ser Ala Pro Pro Ser Lys Ser Val Pro Leu Tyr Gly Ala Leu Gly Leu	
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act cat cat cag tat gat gaa caa gga gcc gcc ggt gtg ttt gct gct	652
Thr His His Gln Tyr Asp Glu Gln Gly Gly Gly Val Phe Ala Ala	
155 160 165 170	
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His Thr Ser Pro Leu Leu Gly Phe His His Gln Leu Gln His His Gln	
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Asn Gln Asn Gln Asn Gln Asp Pro Val Glu Thr Ile Pro Glu Gly Glu	
190 195 200	
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Asn Phe Ser Arg Lys Arg Tyr Arg Ser Val Asp Leu Ser Lys Glu Asn	
205 210 215	

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Asp Asp Arg Lys Gln Asn Glu Asn Lys Ser Leu Lys Glu Ser Glu Thr	
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Ser Gly Pro Thr Ala Ala Pro Met Trp Ala Val Ala Pro Pro Ser Arg	
235 240 245 250	
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Ser Gly Ala Gly Asn Thr Phe Trp Met Leu Pro Val Pro Thr Thr Ala	
255 260 265	
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Gly Asn Gln Met Glu Ser Ser Ser Asn Asn Asn Thr Ala Ala Gly His	
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Arg Ala Pro Pro Met Trp Pro Phe Val Asn Ser Ala Gly Gly Gly Ala	
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Gly Gly Gly Gly Gly Ala Ala Thr His Phe Met Ala Gly Thr Gly Phe	
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Ser Phe Pro Met Asp Gln Tyr Arg Gly Ser Pro Leu Gln Leu Gly Ser	
315 320 325 330	
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Phe Leu Ala Gln Pro Gln Pro Thr Gln Asn Leu Gly Leu Ser Met Pro	
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Asp Ser Asn Leu Gly Met Leu Ala Ala Leu Asn Ser Ala Tyr Ser Arg	
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His Gln Glu Lys Gln Gln Ser Asp His Asp Asp Asp Ser Arg Glu	
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Thr	Lys	Val	Asp	Gly	Arg	Gly	Arg	Arg	Ile	Arg	Met	Pro	Ala	Leu	Cys
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Gly	Glu	Thr	Ile	Glu	Trp	Leu	Leu	Gln	Gln	Ala	Glu	Pro	Ala	Ile	Val
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Val	Ser	Leu	Arg	Ser	Ser	Gly	Ser	Thr	Leu	Ser	Ala	Pro	Pro	Ser	Lys
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Ser	Val	Pro	Leu	Tyr	Gly	Ala	Leu	Gly	Leu	Thr	His	His	Gln	Tyr	Asp
145				150					155					160	
Glu	Gln	Gly	Gly	Gly	Gly	Val	Phe	Ala	Ala	His	Thr	Ser	Pro	Leu	Leu
		165						170						175	
Gly	Phe	His	His	Gln	Leu	Gln	His	His	Gln	Asn	Gln	Asn	Gln	Asn	Gln
		180						185					190		
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	195					200						205			
Tyr	Arg	Ser	Val	Asp	Leu	Ser	Lys	Glu	Asn	Asp	Asp	Arg	Lys	Gln	Asn
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Glu	Asn	Lys	Ser	Leu	Lys	Glu	Ser	Glu	Thr	Ser	Gly	Pro	Thr	Ala	Ala
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Pro	Met	Trp	Ala	Val	Ala	Pro	Pro	Ser	Arg	Ser	Gly	Ala	Gly	Asn	Thr
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Ser Ser Asn Asn Asn Thr Ala Ala Gly His Arg Ala Pro Pro Met Trp
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Pro Phe Val Asn Ser Ala Gly Gly Gly Ala Gly Gly Gly Gly Ala
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Ala Thr His Phe Met Ala Gly Thr Gly Phe Ser Phe Pro Met Asp Gln
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Tyr Arg Gly Ser Pro Leu Gln Leu Gly Ser Phe Leu Ala Gln Pro Gln
 325 330 335

Pro Thr Gln Asn Leu Gly Leu Ser Met Pro Asp Ser Asn Leu Gly Met
 340 345 350

Leu Ala Ala Leu Asn Ser Ala Tyr Ser Arg Gly Gly Asn Ala Asn Ala
 355 360 365

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 Val Thr Thr Pro Ala Pro Ala Asp Thr Pro Ala Pro Ala Pro Ala Glu
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 Ile Pro Ala Pro Ala Pro Ala Pro Thr Pro Ala Asp Val Thr Lys Asp
 35 40 45

gtt gca gag gag aaa att caa aac cca cct ccg gag caa att ttc gat 253
 Val Ala Glu Glu Lys Ile Gln Asn Pro Pro Pro Glu Glu Ile Phe Asp
 50 55 60

gac tcc aaa gcc ctt act gtt gtt gag aaa cct gta gaa gag cct gca 301
 Asp Ser Lys Ala Leu Thr Val Val Glu Lys Pro Val Glu Glu Pro Ala
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 Pro Ala Lys Pro Ala Ser Ala Ser Leu Asp Arg Asp Val Lys Leu Ala
 85 90 95
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 Asp Leu Ser Lys Glu Lys Arg Leu Ser Phe Val Arg Ala Trp Glu Glu
 100 105 110
 agc gaa aag agc aaa gca gag aac aaa gct gag aag aag att gca gat 445
 Ser Glu Lys Ser Lys Ala Glu Asn Lys Ala Glu Lys Lys Ile Ala Asp
 115 120 125
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 Val His Ala Trp Glu Asn Ser Lys Lys Ala Ala Val Glu Ala Gln Leu
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 aag aaa atc gag gag caa cta gag aag aag aaa gca gag tat gca gag 541
 Lys Lys Ile Glu Glu Gln Leu Glu Lys Lys Lys Ala Glu Tyr Ala Glu
 145 150 155 160
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 Arg Met Lys Asn Lys Val Ala Ala Ile His Lys Glu Ala Glu Glu Arg
 165 170 175
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 Arg Ala Met Ile Glu Ala Lys Arg Gly Glu Asp Val Leu Lys Ala Glu
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 Glu Thr Ala Ala Lys Tyr Arg Ala Thr Gly Ile Val Pro Lys Ala Thr
 195 200 205
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 Cys Gly Cys Phe
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 35 40 45
 Val Ala Glu Glu Lys Ile Gln Asn Pro Pro Pro Glu Gln Ile Phe Asp
 50 55 60
 Asp Ser Lys Ala Leu Thr Val Val Glu Lys Pro Val Glu Glu Pro Ala
 65 70 75 80
 Pro Ala Lys Pro Ala Ser Ala Ser Leu Asp Arg Asp Val Lys Leu Ala
 85 90 95
 Asp Leu Ser Lys Glu Lys Arg Leu Ser Phe Val Arg Ala Trp Glu Glu
 100 105 110
 Ser Glu Lys Ser Lys Ala Glu Asn Lys Ala Glu Lys Lys Ile Ala Asp
 115 120 125
 Val His Ala Trp Glu Asn Ser Lys Lys Ala Ala Val Glu Ala Gln Leu
 130 135 140
 Lys Lys Ile Glu Glu Gln Leu Glu Lys Lys Lys Ala Glu Tyr Ala Glu
 145 150 155 160
 Arg Met Lys Asn Lys Val Ala Ala Ile His Lys Glu Ala Glu Glu Arg
 165 170 175
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Glu	Pro	Phe	Gln	Gln	Ile	Val	Gly	Trp	Gly	Asn	Val	Phe	Lys	Ser	Asp	
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atc	aat	gat	cat	agt	ccc	aat	act	gct	act	tcc	tct	att	att	cag	gtt	321
Ile	Asn	Asp	His	Ser	Pro	Asn	Thr	Ala	Thr	Ser	Ser	Ile	Ile	Gln	Val	
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gat	cct	aga	att	gat	gat	cac	aac	aac	aac	atc	aag	ata	aat	tat	gat	369
Asp	Pro	Arg		Asp	Asp	His	Asn	Asn	Asn	Ile	Lys	Ile	Asn	Tyr	Asp	
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Ser	Ser	His	Asn	Gln	Ile	Glu	Ala	Glu	Gln	Pro	Ser	Ser	Asn	Asp	Asn	
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caa	gat	gat	gat	ggc	agg	att	cat	gat	aag	atg	aaa	cgg	cgt	tta	gcg	465
Gln	Asp	Asp	Asp	Gly	Arg	Ile	His	Asp	Lys	Met	Lys	Arg	Arg	Leu	Ala	
	85					90					95					
cag	aac	cga	gaa	gcg	gct	cgc	aaa	agt	cgt	ttg	aga	aag	aag	gct	tat	513
Gln	Asn	Arg	Glu	Ala	Ala	Arg	Lys	Ser	Arg	Leu	Arg	Lys	Lys	Ala	Tyr	
100				105						110				115		
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Val	Gln	Gln	Leu	Glu	Glu	Ser	Arg	Leu	Lys	Leu	Ser	Gln	Leu	Glu	Gln	
				120				125						130		
gaa	ctc	gaa	aag	gtt	aag	cag	cag	ggc	cat	tta	gga	cca	tct	ggg	agt	609
Glu	Leu	Glu	Lys	Val	Lys	Gln	Gln	Gly	His	Leu	Gly	Pro	Ser	Gly	Ser	
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Ile	Asn	Thr	Gly	Ile	Ala	Ser	Phe	Glu	Met	Glu	Tyr	Ser	His	Trp	Leu	
		150				155						160				
caa	gaa	caa	agc	aga	aga	gtt	agc	gaa	cta	cga	aca	gcg	ctt	caa	tct	705
Gln	Glu	Gln	Ser	Arg	Arg	Val	Ser	Glu	Leu	Arg	Thr	Ala	Leu	Gln	Ser	
	165					170					175					
cat	ata	agc	gac	ata	gaa	ctc	aag	atg	cta	gta	gag	agt	tcg	ttg	aac	753
His	Ile	Ser	Asp	Ile	Glu	Leu	Lys	Met	Leu	Val	Glu	Ser	Cys	Leu	Asn	
180					185					190				195		
cat	tac	gct	aat	ctt	ttc	cga	atg	aaa	tcc	gat	gca	gca	aaa	gcc	gat	801
His	Tyr	Ala	Asn	Leu	Phe	Arg	Met	Lys	Ser	Ser	Asp	Ala	Ala	Lys	Ala	
				200					205							

gtt ttc tac ttg ata tgc gga atg tgg cga act tca acc gaa aga ttc 849
 Val Phe Tyr Leu Ile Ser Gly Met Trp Arg Thr Ser Thr Glu Arg Phe
 215 220 225

ttc caa tgg att gga ggg ttt cgt cca tcc gaa ctt tta aac gtt gtg 897
 Phe Gln Trp Ile Gly Gly Phe Arg Pro Ser Glu Leu Leu Asn Val Val
 230 235 240

atg cct tat ctt caa cca tta acg gat caa caa atc ttg gaa gtg aga 945
 Met Pro Tyr Leu Gln Pro Leu Thr Asp Gln Gln Ile Leu Glu Val Arg
 245 250 255

aac ctg caa caa tca tca caa caa gca gag gat gct ctg tct caa ggg 993
 Asn Leu Gln Gln Ser Ser Gln Gln Ala Glu Asp Ala Leu Ser Gln Gly
 260 265 270 275

att gat aaa ctt caa cag agt tta gct gaa agc att gtg att gat gcg 1041
 Ile Asp Lys Leu Gln Gln Ser Leu Ala Glu Ser Ile Val Ile Asp Ala
 280 285 290

gtt atc gag tcc acg cat tat ccc act cac atg gct gca gct ata gag 1089
 Val Ile Glu Ser Thr His Tyr Pro Thr His Met Ala Ala Ile Glu
 295 300 305

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 Asn Leu Gln Ala Leu Glu Gly Phe Val Asn Gln Ala Asp His Leu Arg
 310 315 320

caa caa act ttg caa caa atg gcg aag atc tta acg aca aga caa tgc 1185
 Gln Gln Thr Leu Gln Gln Met Ala Lys Ile Leu Thr Thr Arg Gln Ser
 325 330 335

gct cga ggt tta cta gct tta gga gag tat ctt cat aga ctt cgt gct 1233
 Ala Arg Gly Leu Leu Ala Leu Gly Glu Tyr Leu His Arg Leu Arg Ala
 340 345 350 355

ctt agt tct ctt tgg gca gct cgt cca caa gaa cca act taaaagagga 1282
 Leu Ser Ser Leu Trp Ala Ala Arg Pro Gln Glu Pro Thr
 360 365

acttattaaa actttaaaaa caagaaacag cagaatcaaa agtcttgaag aagcatactc 1342

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ctcttgatta gaactttatg gtttttgctt tatgaagtat ctctccagag aagattgtaa 1462

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 35 40 45

Ile Gln Val Asp Pro Arg Ile Asp Asp His Asn Asn Asn Ile Lys Ile
 50 55 60

Asn Tyr Asp Ser Ser His Asn Gln Ile Glu Ala Glu Gln Pro Ser Ser
 65 70 75 80

Asn Asp Asn Gln Asp Asp Asp Gly Arg Ile His Asp Lys Met Lys Arg
 85 90 95

Arg Leu Ala Gln Asn Arg Glu Ala Ala Arg Lys Ser Arg Leu Arg Lys
 100 105 110

Lys Ala Tyr Val Gln Gln Leu Glu Glu Ser Arg Leu Lys Leu Ser Gln
 115 120 125

Leu Glu Gln Glu Leu Glu Lys Val Lys Gln Gln Gly His Leu Gly Pro
 130 135 140

Ser Gly Ser Ile Asn Thr Gly Ile Ala Ser Phe Glu Met Glu Tyr Ser
 145 150 155 160

His Trp Leu Gln Glu Gln Ser Arg Arg Val Ser Glu Leu Arg Thr Ala
 165 170 175

Leu Gln Ser His Ile Ser Asp Ile Glu Leu Lys Met Leu Val Glu Ser
 180 185 190

Cys Leu Asn His Tyr Ala Asn Leu Phe Arg Met Lys Ser Asp Ala Ala
 195 200 205

Lys Ala Asp Val Phe Tyr Leu Ile Ser Gly Met Trp Arg Thr Ser Thr
 210 215 220

Glu Arg Phe Phe Gln Trp Ile Gly Gly Phe Arg Pro Ser Glu Leu Leu
 225 230 235 240

Asn Val Val Met Pro Tyr Leu Gln Pro Leu Thr Asp Gln Gln Ile Leu
 245 250 255

Glu Val Arg Asn Leu Gln Gln Ser Ser Gln Gln Ala Glu Asp Ala Leu
 260 265 270

Ser Gln Gly Gly Ile Asp Lys Leu Gln Gln Ser Leu Ala Glu Ser Ile Val
 275 280 285

Ile Asp Ala Val Ile Glu Ser Thr His Tyr Pro Thr His Met Ala Ala
 290 295 300

Ala Ile Glu Asn Leu Gln Ala Leu Glu Gly Phe Val Asn Gln Ala Asp
305 310 315 320

His Leu Arg Gln Gln Thr Leu Gln Gln Met Ala Lys Ile Leu Thr Thr
325 330 335

Arg Gln Ser Ala Arg Gly Leu Leu Ala Leu Gly Glu Tyr Leu His Arg
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Met Gln Gln Gln Asp Tyr Phe Asn Leu Asn Asn Tyr Tyr Asn Asn Leu
15 20 25

aac cct tca acc aat aac aac aac ctc aat atc ctc caa tac cct caa 146
Asn Pro Ser Thr Asn Asn Asn Asn Leu Asn Ile Leu Gln Tyr Pro Gln
30 35 40

att caa gaa ctc aac cta caa tct ccg gta agc aac aac tcc aca act 194
Ile Gln Glu Leu Asn Leu Gln Ser Pro Val Ser Asn Asn Ser Thr Thr
45 50 55 60

tcc gat gac gca act gaa gaa atc ttc gtc atc aac gag agg aag caa 242
Ser Asp Asp Ala Thr Glu Glu Ile Phe Val Ile Asn Glu Arg Lys Gln
65 70 75

aga cgt atg gta tct aac aga gag tca gca aga aga tca aga atg aga 290
Arg Arg Met Val Ser Asn Arg Glu Ser Ala Arg Arg Ser Arg Met Arg
80 85 90

aag caa aga cac tta gat gag ctt ctc tca cag gtt gct tgg ctt cga 338
Lys Gln Arg His Leu Asp Glu Leu Ser Gln Val Ala Trp Leu Arg
95 100 105

agc gag aac cac cag ctt tta gat aag ctt aac caa gtc tcc gac aac 386
Ser Glu Asn His Gln Leu Asp Lys Leu Asn Gln Val Ser Asp Asn
110 115 120

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aat gat ctt gtt att caa gag aac tcg agt ctt aaa gaa gaa aac ttg 434
Asn Asp Leu Val Ile Gln Glu Asn Ser Ser Leu Lys Glu Glu Asn Leu
125 130 135 140

gag ctt cgt cag gtt atc aca tcc atg aag aag ctt gga gga ggc ata 482
Glu Leu Arg Gln Val Ile Thr Ser Met Lys Lys Leu Gly Gly Gly Ile
145 150 155

cat gac aaa tat tct tct ccg tgg tct atg gat gaa ttg gat caa gac 530
His Asp Lys Tyr Ser Ser Pro Ser Ser Met Asp Glu Leu Asp Gln Asp
160 165 170

ttt tct tct atc aca gat gat cca aga act cat cat cca tca 572
Phe Ser Ser Ile Thr Asp Asp Pro Arg Thr His His Pro Ser
175 180 185

tgagttgttc tgatcgagaa aaacattact tcaagtttct gcctctaato ttatctattt 632
tttttttttg gtatcacttt ttaaaccggt taactacgta ccaaagtttg ggttttattt 692
gtttttctgt tgtttttgtca gaagataatt aaatgatgga tatttgaaaa aaaaaaaaaa 752
aaaaaaaaa 759

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<213> Arabidopsis thaliana

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<223> G630

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Asn Asn Asn Asn Leu Asn Ile Leu Gln Tyr Pro Gln Ile Gln Glu Leu
35 40 45
Asn Leu Gln Ser Pro Val Ser Asn Asn Ser Thr Thr Ser Asp Asp Ala
50 55 60
Thr Glu Glu Ile Phe Val Ile Asn Glu Arg Lys Gln Arg Arg Met Val
65 70 75 80
Ser Asn Arg Glu Ser Ala Arg Arg Ser Arg Met Arg Lys Gln Arg His
85 90 95
Leu Asp Glu Leu Leu Ser Gln Val Ala Trp Leu Arg Ser Glu Asn His
100 105 110
Gln Leu Leu Asp Lys Leu Asn Gln Val Ser Asp Asn Asn Asp Leu Val
115 120 125

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gcc aat gaa tca gaa caa gcc tct ctt gct tct tcc aaa gct aca cca 387
Ala Asn Glu Ser Glu Gln Ala Ser Leu Ala Ser Ser Lys Ala Thr Pro
110 115 120

atg atg agc agt gct ata aca agt gga tct gag ctc tct ggt gat gaa 435
Met Met Ser Ser Ala Ile Thr Ser Gly Ser Glu Leu Ser Gly Asp Glu
125 130 135

gaa gaa gct gat ggt gaa act aat atg aac cct act aat gtt aaa cgc 483
Glu Glu Ala Asp Gly Glu Thr Asn Met Asn Pro Thr Asn Val Lys Arg
140 145 150

gtt aaa agg atg ctc tct aat aga gaa tca gct aga cgg tcc aga aga 531
Val Lys Arg Met Leu Ser Asn Arg Glu Ser Ala Arg Arg Ser Arg Arg
155 160 165 170

aga aag caa gca cac ttg agt gag cta gag aca caa gtt tca cag ctt 579
Arg Lys Gln Ala His Leu Ser Glu Leu Glu Thr Gln Val Ser Gln Leu
175 180 185

cgt gta gag aat tca aaa ctc atg aag ggt ctc act gat gta act caa 627
Arg Val Glu Asn Ser Lys Leu Met Lys Gly Leu Thr Asp Val Thr Gln
190 195 200

aca ttc aat gat gca tct gta gaa aac aga gtt tta aaa gcc aat att 675
Thr Phe Asn Asp Ala Ser Val Glu Asn Arg Val Leu Lys Ala Asn Ile
205 210 215

gag aca cta cga gca aag gtg aaa atg gct gaa gag aca gtg aag aga 723
Glu Thr Leu Arg Ala Lys Val Lys Met Ala Glu Glu Thr Val Lys Arg
220 225 230

ctc act ggc ttt aac cca atg ttc cac aat atg cct cag att gtt tca 771
Leu Thr Gly Phe Asn Pro Met Phe His Asn Met Pro Gln Ile Val Ser
235 240 245 250

act gtc tct ctt cct tca gag aca tca aat tct cca gac act aca agc 819
Thr Val Ser Leu Pro Ser Glu Thr Ser Asn Ser Pro Asp Thr Thr Ser
255 260 265

agc caa gtg act aca cca gag atc att agc tcg ggg aac aaa ggc aag 867
Ser Gln Val Thr Thr Pro Glu Ile Ile Ser Ser Gly Asn Lys Gly Lys
270 275 280

gcc ttg ata ggg tgc aag atg aac aga aca gct tcg atg cgt agt gtt 915
Ala Leu Ile Gly Cys Lys Met Asn Arg Thr Ala Ser Met Arg Ser Val
285 290 295

gag agc ttg gaa cat ctg cag aaa cgt att cga agc gtt ggg gat cag 963
Glu Ser Leu Glu His Leu Lys Arg Ile Arg Ser Val Gly Asp Gln
300 305 310

tagctgttaa agaagaatct tgatttgtaa cattaatctt aagacatatg ttaaagacaa 1023

aattgtgtat gtttttggcg gcgcgaatt cctgcag 1060

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<213> Arabidopsis thaliana

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<223> G735

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Phe Asn Arg Phe Ile Gln Glu Ser Ser Ala Ala Ala Asp Asp Gly Glu
          35          40          45

Ser Thr Thr Ala Cys Gly Val Ser Val Ser Ser Pro Asn Val Pro
  50          55          60

Val Asp Ser Glu Glu Tyr Arg Ala Phe Leu Lys Ser Lys Leu Asn Leu
  65          70          75          80

Ala Cys Ala Ala Val Ala Met Lys Arg Gly Thr Phe Ile Lys Pro Gln
          85          90          95

Asp Thr Ser Gly Arg Ser Asp Asn Gly Gly Ala Asn Glu Ser Glu Gln
          100         105         110

Ala Ser Leu Ala Ser Ser Lys Ala Thr Pro Met Met Ser Ser Ala Ile
  115         120         125

Thr Ser Gly Ser Glu Leu Ser Gly Asp Glu Glu Glu Ala Asp Gly Glu
  130         135         140

Thr Asn Met Asn Pro Thr Asn Val Lys Arg Val Lys Arg Met Leu Ser
  145         150         155         160

Asn Arg Glu Ser Ala Arg Arg Ser Arg Arg Arg Lys Gln Ala His Leu
          165         170         175

Ser Glu Leu Glu Thr Gln Val Ser Gln Leu Arg Val Glu Asn Ser Lys
  180         185         190

Leu Met Lys Gly Leu Thr Asp Val Thr Gln Thr Phe Asn Asp Ala Ser
  195         200         205

Val Glu Asn Arg Val Leu Lys Ala Asn Ile Glu Thr Leu Arg Ala Lys
  210         215         220

Val Lys Met Ala Glu Glu Thr Val Lys Arg Leu Thr Gly Phe Asn Pro
  225         230         235         240

Met Phe His Asn Met Pro Gln Ile Val Ser Thr Val Ser Leu Pro Ser
          245         250         255

Glu Thr Ser Asn Ser Pro Asp Thr Thr Ser Ser Gln Val Thr Thr Pro
          260         265         270

Glu Ile Ile Ser Ser Gly Asn Lys Gly Lys Ala Leu Ile Gly Cys Lys
  275         280         285

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Met Asn Arg Thr Ala Ser Met Arg Ser Val Glu Ser Leu Glu His Leu
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Gln Lys Arg Ile Arg Ser Val Gly Asp Gln
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<222> (214) .. (1440)

<223> G1034

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ttttcttcgcg catcttttgtt ttagegcaac tgcattgtttt tggttatccc ttcaacataa 120

ttgcatatta atttctttca ttttaataacc tgatacaaaa aagtcgctct aatatataat 180

ttattctcaa actttcaata cactccacac agc atg gaa act gta cga tat cca 234
Met Glu Thr Val Arg Tyr Pro
1 5

aag tac gaa aat tgc cgc gcc gag acc atg gtg gaa agc ttc gtg tgc 282
Lys Tyr Glu Asn Ser Pro Ala Glu Thr Met Val Glu Ser Phe Val Ser
10 15 20

aca cct tct tca ttt cat aac cct cca ctt ttc gac aac aac tta aac 330
Thr Pro Ser Ser Phe His Asn Pro Pro Leu Phe Asp Asn Asn Leu Asn
25 30 35

cct gta gat ggg ttt tcc cca caa tca ttt gac cgt gac tac aat ttc 378
Pro Val Asp Gly Phe Ser Pro Gln Ser Phe Asp Arg Asp Tyr Asn Phe
40 45 50 55

aac ggt agt tta tca ggg ctg aac ctt ccc gag aaa aaa ccc atc aaa 426
Asn Gly Ser Leu Ser Gly Leu Asn Leu Pro Glu Lys Lys Pro Ile Lys
60 65 70

aag cgc aag tct tgg gga cag caa ctt ccc gaa ccc aaa aca aac ctt 474
Lys Arg Lys Ser Trp Gly Gln Gln Leu Pro Glu Pro Lys Thr Asn Leu
75 80 85

cct cgc agg aag cgc gca aag act caa gat gaa aaa gag caa cgg cgt 522
Pro Pro Arg Lys Arg Ala Lys Thr Gln Asp Glu Lys Glu Gln Arg Arg
90 95 100

gtt gag cgc gtc cta cgc aat cgt aga gcg gcc caa tca tca cga gaa 570
Val Glu Arg Val Leu Arg Asn Arg Arg Ala Ala Gln Ser Ser Arg Glu
105 110 115

cga aaa cgc cag gag gtc gag gct ttg gaa gtc gag aaa cga gct att Arg Lys Arg Gln Glu Val Glu Ala Leu Glu Val Glu Lys Arg Ala Ile 120 125 130 135	618
gag cgc aaa aac atg gat ctt gag atg cgc tta gca gac atg gaa gca Glu Arg Lys Asn Met Asp Leu Glu Met Arg Leu Ala Asp Met Glu Ala 140 145 150	666
aag tac tac ctt ctt caa cag gaa ctg aaa cga gcc agt ggt tac aac Lys Tyr Tyr Leu Leu Gln Gln Glu Leu Lys Arg Ala Ser Gly Tyr Asn 155 160 165	714
aag aca aac ttt ctt tcc tac tct gat tct tca act cca gac atc tcc Lys Thr Asn Phe Leu Ser Tyr Ser Asp Ser Ser Thr Pro Asp Ile Ser 170 175 180	762
gaa gat tca caa tta tca cct ttg act ttc tct aag caa ctc ttc aac Glu Asp Ser Gln Leu Ser Pro Leu Thr Phe Ser Lys Gln Leu Phe Asn 185 190 195	810
gct caa gat gaa ttg tgt cga cca ata agt cct cag tca atc ggt cag Ala Gln Asp Glu Leu Cys Arg Pro Ile Ser Pro Gln Ser Ile Gly Pro 200 205 210 215	858
ctg act tca aga acc gtt gac cct tct aca ctc tca cct aag tct tta Leu Thr Ser Arg Thr Val Asp Pro Ser Thr Leu Ser Pro Lys Ser Leu 220 225 230	906
tct tct ccc gat tca tcc aat tct aat tct tcc gac atg aca caa cat Ser Ser Pro Asp Ser Ser Asn Ser Asn Ser Ser Asp Met Thr Gln His 235 240 245	954
cct gcc gtg gtg ttg tgc gac ctg cag tgt cag tog gaa ctg ggt cag Pro Ala Val Val Leu Cys Asp Leu Gln Cys Gln Ser Glu Leu Gly Gln 250 255 260	1002
cct tgg atg aat tgc aca tat ctt tct ttg aga acg aaa gct ctg aaa Pro Trp Met Asn Ser Thr Tyr Leu Ser Leu Arg Thr Lys Ala Leu Lys 265 270 275	1050
tta tgc gta act tac ctt att aca atg tta aca act ttt ttg att gtc Leu Ser Val Thr Tyr Leu Ile Thr Met Leu Thr Thr Phe Leu Ile Val 280 285 290 295	1098
ctc gga aac ctg aat cag aat atc atg ttt tta atg acg aga ttt ctc Leu Gly Asn Leu Asn Gln Asn Ile Met Phe Leu Met Thr Arg Phe Leu 300 305 310	1146
ctc aca cca acg tat ttt att cag agg atg aaa ata ttc ggg gac aga Leu Thr Pro Thr Tyr Phe Ile Gln Arg Met Lys Ile Phe Gly Asp Arg 315 320 325	1194
acg acg gtg ttt tgc atg aat ttg tgc tat gtg atc ttc tca acg atg Thr Thr Val Phe Ser Met Asn Leu Ser Tyr Val Ile Phe Ser Thr Met 330 335 340	1242

aaa ctc tat caa acg aga gtc tgc att cgg atc agc ttg ctg gga cga 1290
 Lys Leu Tyr Gln Thr Arg Val Cys Ile Arg Ile Ser Leu Leu Gly Arg
 345 350 355

cga caa gcc tgc agc cgc aat ttg gcg cgt tct cta atg aat gcg acg 1338
 Arg Gln Ala Cys Ser Arg Asn Leu Ala Arg Ser Leu Met Asn Ala Thr
 360 365 370 375

atg gcg gca ttg cgg ttt gag tcc aaa cag cga ctt ttt cgc aat ttt 1386
 Met Ala Ala Leu Arg Phe Glu Ser Lys Gln Arg Leu Phe Arg Asn Phe
 380 385 390

ctc tct act gta gcg ctt cag att tct cga aga tcc tcc cac ttt tta 1434
 Leu Ser Thr Val Ala Leu Gln Ile Ser Arg Arg Ser Ser His Phe Leu
 395 400 405

tgg tac tgaataact cgaagacact aaactgaacg agagaaatga gaagcgatgg 1490
 Trp Tyr

ttccaatttc aaatgtcgac cttaacttat tgtgttcgat tgaggattag taaaaatcta 1550

atggtatatt tagaataata ttcataaaga aaattttataa taaatctact caatacattg 1610

aaaaattagc ttttggattt ttactgctta ggatataga atggtcacag ttcatagctg 1670

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Leu Phe Asp Asn Asn Leu Asn Pro Val Asp Gly Phe Ser Pro Gln Ser
 35 40 45

Phe Asp Arg Asp Tyr Asn Phe Asn Gly Ser Leu Ser Gly Leu Asn Leu
 50 55 60

Pro Glu Lys Lys Pro Ile Lys Lys Arg Lys Ser Trp Gly Gln Gln Leu
 65 70 75 80

Pro Glu Pro Lys Thr Asn Leu Pro Pro Arg Lys Arg Ala Lys Thr Gln
 85 90 95

Asp Glu Lys Glu Gln Arg Arg Val Glu Arg Val Leu Arg Asn Arg Arg
 100 105 110
 Ala Ala Gln Ser Ser Arg Glu Arg Lys Arg Gln Glu Val Glu Ala Leu
 115 120 125
 Glu Val Glu Lys Arg Ala Ile Glu Arg Lys Asn Met Asp Leu Glu Met
 130 135 140
 Arg Leu Ala Asp Met Glu Ala Lys Tyr Tyr Leu Gln Gln Glu Leu
 145 150 155 160
 Lys Arg Ala Ser Gly Tyr Asn Lys Thr Asn Phe Leu Ser Tyr Ser Asp
 165 170 175
 Ser Ser Thr Pro Asp Ile Ser Glu Asp Ser Gln Leu Ser Pro Leu Thr
 180 185 190
 Phe Ser Lys Gln Leu Phe Asn Ala Gln Asp Glu Leu Cys Arg Pro Ile
 195 200 205
 Ser Pro Gln Ser Ile Gly Pro Leu Thr Ser Arg Thr Val Asp Pro Ser
 210 215 220
 Thr Leu Ser Pro Lys Ser Leu Ser Ser Pro Asp Ser Ser Asn Ser Asn
 225 230 235 240
 Ser Ser Asp Met Thr Gln His Pro Ala Val Leu Cys Asp Leu Gln
 245 250 255
 Cys Gln Ser Glu Leu Gly Gln Pro Trp Met Asn Ser Thr Tyr Leu Ser
 260 265 270
 Leu Arg Thr Lys Ala Leu Lys Leu Ser Val Thr Tyr Leu Ile Thr Met
 275 280 285
 Leu Thr Thr Phe Leu Ile Val Leu Gly Asn Leu Asn Gln Asn Ile Met
 290 295 300
 Phe Leu Met Thr Arg Phe Leu Leu Thr Pro Thr Tyr Phe Ile Gln Arg
 305 310 315 320
 Met Lys Ile Phe Gly Asp Arg Thr Thr Val Phe Ser Met Asn Leu Ser
 325 330 335
 Tyr Val Ile Phe Ser Thr Met Lys Leu Tyr Gln Thr Arg Val Cys Ile
 340 345 350
 Arg Ile Ser Leu Leu Gly Arg Arg Gln Ala Cys Ser Arg Asn Leu Ala
 355 360 365
 Arg Ser Leu Met Asn Ala Thr Met Ala Ala Leu Arg Phe Glu Ser Lys
 370 375 380
 Gln Arg Leu Phe Arg Asn Phe Leu Ser Thr Val Ala Leu Gln Ile Ser
 385 390 395 400

00704513-001909

Arg Arg Ser Ser His Phe Leu Trp Tyr
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gcgtcttaat catagtactt aattttctct gtgtgtttta at atg aat aat aaa 114
Met Asn Asn Lys
1

act gaa atg gga tct tcc aca agt gga aat tgc tgc tgc gtt tca acc 162
Thr Glu Met Gly Ser Ser Thr Ser Gly Asn Cys Ser Ser Val Ser Thr
5 10 15 20

act ggt tta gct aac tcc ggt tca gaa tct gat ctc cgg caa cgt gat 210
Thr Gly Leu Ala Asn Ser Gly Ser Glu Ser Asp Leu Arg Gln Arg Asp
25 30 35

cta atc gac gag cgg aag aga aag agg aaa cag tgc aac aga gaa tct 258
Leu Ile Asp Glu Arg Lys Arg Lys Arg Lys Gln Ser Asn Arg Glu Ser
40 45 50

gcg agg agg tgc agg atg agg aag cag aag cat ttg gat gat ctc act 306
Ala Arg Arg Ser Arg Met Arg Lys Gln Lys His Leu Asp Asp Leu Thr
55 60 65

gct cag gtg act cat cta cgt aaa gaa aac gct cag atc gtc gcc gga 354
Ala Gln Val Thr His Leu Arg Lys Glu Asn Ala Gln Ile Val Ala Gly
70 75 80

atc gcc gtc acg acg cag cac tac gtc act atc gag gcg gag aac gac 402
Ile Ala Val Thr Thr Gln His Tyr Val Thr Ile Glu Ala Glu Asn Asp
85 90 95 100

att ctc aga gct cag gtt ctt gaa ctt aac cac cgt ctc caa tct ctt 450
Ile Leu Arg Ala Gln Val Leu Glu Leu Asn His Arg Leu Gln Ser Leu
105 110 115

aac gag atc gtt gat ttc gtc gaa tct tct tca gga ttc ggt atg 498
Asn Glu Ile Val Asp Phe Val Glu Ser Ser Ser Ser Gly Phe Gly Met
120 125 130

gag acc ggt cag gga tta ttc gac ggt gga tta ttc gac gcc gtg atg 546
Glu Thr Gly Gln Gly Leu Phe Asp Gly Gly Leu Phe Asp Gly Val Met
135 140 145

aat cct atg aat cta ggg ttt tat aat caa cca atc atg gct tct gct 594
 Asn Pro Met Asn Leu Gly Phe Tyr Asn Gln Pro Ile Met Ala Ser Ala
 150 155 160

tct act gct ggt gat gtt ttc aac tgt tagaaaaactt cacatcatta 641
 Ser Thr Ala Gly Asp Val Phe Asn Cys
 165 170

tcacgtgag tgagactaat catcgacgca ggggtaaaaac tgtaattttt cttataaatt 701
 atgtgatgat gctttgtttc tttattttat aagatggtta attagtgttt aaaactgatt 761
 gtaatgatag acagtgtgaag aaatgtgtga tatcatggag atgggtgatgt gagtttggtta 821
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 tttcttaaaa aaaaaaaaaa aa 903

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Arg Gln Arg Asp Leu Ile Asp Glu Arg Lys Arg Lys Arg Lys Gln Ser
 35 40 45

Asn Arg Glu Ser Ala Arg Arg Ser Arg Met Arg Lys Gln Lys His Leu
 50 55 60

Asp Asp Leu Thr Ala Gln Val Thr His Leu Arg Lys Glu Asn Ala Gln
 65 70 75 80

Ile Val Ala Gly Ile Ala Val Thr Thr Gln His Tyr Val Thr Ile Glu
 85 90 95

Ala Glu Asn Asp Ile Leu Arg Ala Gln Val Leu Glu Leu Asn His Arg
 100 105 110

Leu Gln Ser Ser Leu Asn Glu Ile Val Asp Phe Val Glu Ser Ser Ser Ser
 115 120 125

Gly phe Gly Met Glu Thr Gly Gln Gly Leu Phe Asp Gly Gly Leu Phe
 130 135 140

Asp Gly Val Met Asn Pro Met Asn Leu Gly Phe Tyr Asn Gln Pro Ile
 145 150 155 160

Met Ala Ser Ala Ser Thr Ala Gly Asp Val Phe Asn Cys
165 170

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<212> DNA
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<222> (5)..(889)
<223> G1048

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1 5 10 15

ttc ttc ttc gat ttc gat cct tca atc gta att gat tct ctt cgg gcg 97
Phe Phe Phe Asp Phe Asp Pro Ser Ile Val Ile Asp Ser Leu Pro Ala 30
20 25 30

gag gat ttt ctt cag tct tca cgg gat tca tgg atc gga gaa atc gag 145
Glu Asp Phe Leu Gln Ser Ser Pro Asp Ser Trp Ile Gly Glu Ile Glu 45
35 40 45

aat caa ttg atg aac gat gag aat cat caa gag gag agt ttt gtg gaa 193
Asn Gln Leu Met Asn Asp Glu Asn His Gln Glu Glu Ser Phe Val Glu 60
50 55 60

ttg gat cag caa tcg gtt tca gat ttc ata gcg gat cta ctc gtt gat 241
Leu Asp Gln Gln Ser Val Ser Asp Phe Ile Ala Asp Leu Leu Val Asp 75
65 70 75

tat cca act agc gat tct ggc tcc gtt gat ttg gcg gct gat aaa gtt 289
Tyr Pro Thr Ser Asp Ser Gly Ser Val Asp Leu Ala Ala Asp Lys Val 95
80 85 90 95

cta acc gtc gat tct ccc gcc gcc gct gat gat tcc ggg aag gag aat 337
Leu Thr Val Asp Ser Pro Ala Ala Ala Asp Asp Ser Gly Lys Glu Asn 110
100 105 110

tcg gat ttg gtt gtt gag aag aag tct aat gat tct ggt agc gag att 385
Ser Asp Leu Val Val Glu Lys Lys Ser Asn Asp Ser Gly Ser Glu Ile 125
115 120 125

cat gat gat gat gac gaa gaa gga gac gat gat gct gtg gct aaa aaa 433
His Asp Asp Asp Glu Glu Gly Asp Asp Asp Ala Val Ala Lys Lys 140
130 135 140

cga aga agg aga gta aga aat aga gat gcg gcg gtt aga tcg aga gag 481
Arg Arg Arg Arg Val Arg Asn Arg Asp Ala Ala Val Arg Ser Arg Glu 155
145 150 155

agg aag aag gaa tat gta caa gat tta gag aag aag agt aag tat ctc 529
Arg Lys Lys Glu Tyr Val Gln Asp Leu Glu Lys Lys Ser Lys Tyr Leu 175
160 165 170 175

gaa aga gaa tgc ttg aga cta gga cgt atg ctt gag tgc ttc gtt gct 577
 Glu Arg Glu Cys Leu Arg Leu Gly Arg Met Leu Glu Cys Phe Val Ala
 180 185 190

gaa aac cag tct cta cgt tac tgt ttg caa aag ggt aat ggc aat aat 625
 Glu Asn Gln Ser Leu Arg Tyr Cys Leu Gln Lys Gly Asn Gly Asn Asn
 195 200 205

act acc atg atg tgc aag cag gag tct gct gtg ctc ttg ttg gaa tcc 673
 Thr Thr Met Met Ser Lys Gln Glu Ser Ala Val Leu Leu Glu Ser
 210 215 220

ctg ctg ttg ggt tcc ctg ctt tgg ctt ctg gga gta aac ttc att tgc 721
 Leu Leu Leu Gly Ser Leu Leu Trp Leu Leu Gly Val Asn Phe Ile Cys
 225 230 235

cta ttc cct tat atg tcc cac aca aag tgt tgc ctc cta cgt cca gaa 769
 Leu Phe Pro Tyr Met Ser His Thr Lys Cys Cys Leu Leu Arg Pro Glu
 240 245 250 255

cca gaa aag ctg gtt cta aac ggg ctc ggg agt agt agc aaa cgg tct 817
 Pro Glu Lys Leu Val Leu Asn Gly Leu Gly Ser Ser Ser Lys Pro Ser
 260 265 270

tat acc ggc gtt agt cgg aga tgt aag ggt tgc agg cct agg atg aaa 865
 Tyr Thr Gly Val Ser Arg Arg Cys Lys Gly Ser Arg Pro Arg Met Lys
 275 280 285

tac caa atc tta acc ctt gcg gcg tgacaacgcc ttttttaact gcttcttttg 919
 Tyr Gln Ile Leu Thr Leu Ala Ala
 290 295

cgcattttga gttgtagatg agtgtctttt agttttctct ctcttgtttt gtatttcgct 979
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 <211> 295
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G1048

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Asp Phe Leu Gln Ser Ser Pro Asp Ser Trp Ile Gly Glu Ile Glu Asn
 35 40 45

Gln Leu Met Asn Asp Glu Asn His Gln Glu Glu Ser Phe Val Glu Leu
 50 55 60

Asp Gln Gln Ser Val Ser Asp Phe Ile Ala Asp Leu Leu Val Asp Tyr
 65 70 75 80
 Pro Thr Ser Asp Ser Gly Ser Val Asp Leu Ala Ala Asp Lys Val Leu
 85 90 95
 Thr Val Asp Ser Pro Ala Ala Ala Asp Asp Ser Gly Lys Glu Asn Ser
 100 105 110
 Asp Leu Val Val Glu Lys Lys Ser Asn Asp Ser Gly Ser Glu Ile His
 115 120 125
 Asp Asp Asp Asp Glu Glu Gly Asp Asp Asp Ala Val Ala Lys Lys Arg
 130 135 140
 Arg Arg Arg Val Arg Asn Arg Asp Ala Ala Val Arg Ser Arg Glu Arg
 145 150 155 160
 Lys Lys Glu Tyr Val Gln Asp Leu Glu Lys Lys Ser Lys Tyr Leu Glu
 165 170 175
 Arg Glu Cys Leu Arg Leu Gly Arg Met Leu Glu Cys Phe Val Ala Glu
 180 185 190
 Asn Gln Ser Leu Arg Tyr Cys Leu Gln Lys Gly Asn Gly Asn Asn Thr
 195 200 205
 Thr Met Met Ser Lys Gln Glu Ser Ala Val Leu Leu Leu Glu Ser Leu
 210 215 220
 Leu Leu Gly Ser Leu Leu Trp Leu Leu Gly Val Asn Phe Ile Cys Leu
 225 230 235 240
 Phe Pro Tyr Met Ser His Thr Lys Cys Cys Leu Leu Arg Pro Glu Pro
 245 250 255
 Glu Lys Leu Val Leu Asn Gly Leu Gly Ser Ser Ser Lys Pro Ser Tyr
 260 265 270
 Thr Gly Val Ser Arg Arg Cys Lys Gly Ser Arg Pro Arg Met Lys Tyr
 275 280 285
 Gln Ile Leu Thr Leu Ala Ala
 290 295

<210> 163

<211> 1421

<212> DNA

<213> Arabidopsis thaliana

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<221> CDS

<222> (17)..(1126)

<223> G1058

<400> 163

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			1				5					10			
gct gac	gaa gct	cag gcc	atg gcc	atg act	tct gcg	cca gct	gct aca								100
Ala Glu	Glu Ala	Gln Ala	Met Ala	Met Thr	Ser Ala	Pro Ala	Ala Thr								
	15		20			25									
gcg gta	gcg caa	cct ggt	gct ggt	atc cca	ccc cca	ggg ggg	aat etc								148
Ala Val	Ala Ala	Gln Pro	Gly Ala	Gly Ile	Pro Pro	Gly Gly	Asn Leu								
	30		35			40									
cag agg	caa ggt	tcg ttg	acg ttg	cct aga	aca att	agt cag	aag act								196
Gln Arg	Gln Gly	Ser Ser	Leu Thr	Pro Arg	Thr Thr	Ile Ser	Gln Lys								
	45		50			55									
ggt gat	gag gtg	tgg aaa	tgt ttg	atc acc	aag gat	ggg aat	atg gaa								244
Val Asp	Glu Val	Trp Trp	Lys Cys	Leu Ile	Thr Lys	Asp Gly	Asn Met								
		65			70		75								
ggt agc	agc gga	ggc ggt	ggt gag	tcg aat	gtg cct	cct gga	agg caa								292
Gly Ser	Ser Ser	Gly Gly	Gly Gly	Glu Ser	Asn Val	Pro Pro	Gly Arg								
	80			85			90								
cag act	tta ggg	gaa atg	aca ctt	gaa gaa	ttt ctg	ttc cgt	gct ggg								340
Gln Thr	Leu Gly	Glu Met	Thr Thr	Glu Glu	Phe Phe	Leu Arg	Ala Gly								
	95		100			105									
ggt gta	aga gaa	gat aac	tgt ggt	caa cag	atg ggt	cag gtc	aac gga								388
Val Val	Arg Glu	Asp Asp	Cys Val	Gln Gln	Met Met	Gly Gln	Val Asn								
	110		115			120									
aac aat	aac aat	ggg ttt	tat ggt	aac agc	act gct	gct ggc	ggc tta								436
Asn Asn	Asn Asn	Gly Phe	Tyr Gly	Asn Ser	Thr Ala	Gly Ala	Gly Leu								
	125		130		135		140								
ggt ttt	gga ttt	ggt cag	cca aat	caa aac	agc ata	aca ttc	aat ggt								484
Gly Phe	Gly Phe	Gly Gln	Pro Asn	Gln Asn	Ser Ser	Ile Thr	Phe Asn								
	145			150			155								
act aat	gat tct	atg atc	ttg aat	cag cca	cct ggt	tta ggg	ctc aaa								532
Thr Asn	Asp Ser	Met Met	Ile Leu	Asn Gln	Pro Pro	Gly Leu	Gly Leu								
	160			165		170									
atg ggt	gga aca	atg cag	cag cag	caa caa	caa caa	cag cag	ttg ctt								580
Met Gly	Gly Thr	Met Gln	Gln Gln	Gln Gln	Gln Gln	Gln Gln	Leu Leu								
	175		180			185									
cag caa	caa cag	cag atg	cag cag	ctg aat	cag cct	cat cca	cag cag								628
Gln Gln	Gln Gln	Gln Met	Gln Gln	Leu Leu	Gln Pro	His Pro	Gln Gln								
	190		195		200										
cgg ctg	cct caa	acc att	ttt cct	aaa caa	gca aac	gta gca	ttt tct								676
Arg Leu	Pro Pro	Gln Thr	Ile Phe	Pro Lys	Gln Gln	Ala Val	Phe Ser								
	205		210		215		220								

gcg cct gtg aat ata acc aac aag ggt ttt gct ggg gct gca aat aat 724
 Ala Pro Val Asn Ile Thr Asn Lys Gly Phe Ala Gly Ala Ala Asn Asn 235
 225

tct atc aac aat aat aat gga tta gct agt tac gga gga acc ggg gtc 772
 Ser Ile Asn Asn Asn Asn Gly Leu Ala Ser Tyr Gly Gly Thr Gly Val 250
 240

act gtt gca gca act tct cca gga aca agc agc gca gaa aat aat tct 820
 Thr Val Ala Ala Thr Ser Pro Gly Thr Ser Ser Ala Glu Asn Asn Ser 265
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tta tca cca gtt ccg tat gtg ctt aat cga gga cga aga agc aat aca 868
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 275

ggt cta gag aag gtt atc gag agg agg caa agg aga atg atc aag aat 916
 Gly Leu Glu Lys Val Ile Glu Arg Arg Gln Arg Arg Met Ile Lys Asn 300
 285

cgg gaa tca gct gct aga tca aga gct cga aag cag gct tat aca ttg 964
 Arg Glu Ser Ala Ala Arg Ser Arg Ala Arg Lys Gln Ala Tyr Thr Leu 315
 305

gaa ctg gaa gcc gaa att gaa aag ctc aag aaa acg aat caa gaa ctg 1012
 Glu Leu Glu Ala Glu Ile Glu Lys Leu Lys Lys Thr Asn Gln Glu Leu 330
 320

cag aaa aaa cag gct gaa atg gtg gaa atg cag aag aat gag ctg aaa 1060
 Gln Lys Lys Gln Ala Glu Met Val Glu Met Gln Lys Asn Glu Leu Lys 345
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gaa acg tcg aag cga ccg tgg ggc agc aaa agg caa tgc ttg aga agg 1108
 Glu Thr Ser Lys Arg Pro Trp Gly Ser Lys Arg Gln Cys Leu Arg Arg 360
 350

aca tta acc gga cca tgg tgaaggatga agcaacaaga acggatgaac 1156
 Thr Leu Thr Gly Pro Trp 370
 365

cagactccta gcttgggatt aatgtaatag gatagtgcata cctgtacagg agattaagag 1216

aaattgagtg aaagatctag gtacagaggt aggagaggt ttctattatg aataaatgac 1276

attttgtgcc ctgacctttg ttagttagg tttagattat cctctgttat tgactatttg 1336

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 35 40 45

Ser Leu Thr Leu Pro Arg Thr Ile Ser Gln Lys Thr Val Asp Glu Val
 50 55 60

Trp Lys Cys Leu Ile Thr Lys Asp Gly Asn Met Glu Gly Ser Ser Gly
 65 70 75 80

Gly Gly Gly Glu Ser Asn Val Pro Pro Gly Arg Gln Gln Thr Leu Gly
 85 90 95

Glu Met Thr Leu Glu Glu Phe Leu Phe Arg Ala Gly Val Val Arg Glu
 100 105 110

Asp Asn Cys Val Gln Gln Met Gly Gln Val Asn Gly Asn Asn Asn Asn
 115 120 125

Gly Phe Tyr Gly Asn Ser Thr Ala Ala Gly Gly Leu Gly Phe Gly Phe
 130 135 140

Gly Gln Pro Asn Gln Asn Ser Ile Thr Phe Asn Gly Thr Asn Asp Ser
 145 150 155 160

Met Ile Leu Asn Gln Pro Pro Gly Leu Gly Leu Lys Met Gly Gly Thr
 165 170 175

Met Gln Gln Gln Gln Gln Gln Gln Leu Leu Gln Gln Gln Gln Gln
 180 185 190

Gln Met Gln Gln Leu Asn Gln Pro His Pro Gln Gln Arg Leu Pro Gln
 195 200 205

Thr Ile Phe Pro Lys Gln Ala Asn Val Ala Phe Ser Ala Pro Val Asn
 210 215 220

Ile Thr Asn Lys Gly Phe Ala Gly Ala Ala Asn Asn Ser Ile Asn Asn
 225 230 235 240

Asn Asn Gly Leu Ala Ser Tyr Gly Gly Thr Gly Val Thr Val Ala Ala
 245 250 255

Thr Ser Pro Gly Thr Ser Ser Ala Glu Asn Asn Ser Leu Ser Pro Val
 260 265 270

Pro Tyr Val Leu Asn Arg Gly Arg Arg Ser Asn Thr Gly Leu Glu Lys
 275 280 285

Val Ile Glu Arg Arg Gln Arg Arg Met Ile Lys Asn Arg Glu Ser Ala
 290 295 300

tct tct aat gca ttt gaa gaa att aag caa gag aaa gta gaa aat tgc 476
Ser Ser Asn Ala Phe Glu Glu Ile Lys Gln Glu Lys Val Glu Asn Cys
70 75 80

aag act att aaa tct gag tct tct gac caa gga aac tct gtg tca aag 524
 Lys Thr Ile Lys Ser Glu Ser Ser Asp Gln Gly Asn Ser Val Ser Lys
 85 90 95

cct act tat gat atc tct act gag aag tgt gtg gtg aac agt tgt ttt 572
 Pro Thr Tyr Asp Ile Ser Thr Glu Lys Cys Val Val Asn Ser Cys Phe
 100 105 110

tca ttt ccg gat agt gac ggc gtt ttg gag cgg act ccg atg tct gat 620
 Ser Phe Pro Asp Ser Asp Gly Val Leu Glu Arg Thr Pro Met Ser Asp
 115 120 125

tac aag aag att cat ggt ttg atg gat gta ggg tgt gaa aac aag aat 668
 Tyr Lys Lys Ile His Gly Leu Met Asp Val Gly Cys Glu Asn Lys Asn
 130 135 140 145

gta aat aat ggg ttc gag caa gga gaa gca acc gat cgc gtg ggt gat 716
 Val Asn Asn Gly Phe Glu Gln Gly Glu Ala Thr Asp Arg Val Gly Asp
 150 155 160

gga ggc tta gtc act gat act tgc aac tta gag gat gca act gcg tta 764
 Gly Gly Leu Val Thr Asp Thr Cys Asn Leu Glu Asp Ala Thr Ala Leu
 165 170 175

ggt ctg cag ttt ccg aaa tca gtc tgt gtg ggt ggt gat tta aaa tca 812
 Gly Leu Gln Phe Pro Lys Ser Val Cys Val Gly Gly Asp Leu Lys Ser
 180 185 190

cca tcc acc ttg gat atg acc cct aat ggt tcc tat gct aga cat ggg 860
 Pro Ser Thr Leu Asp Met Thr Pro Asn Gly Ser Tyr Ala Arg His Gly
 195 200 205

aac cat act aac cta ggt aga aaa gat gat gat gaa aaa ttc tat agt 908
 Asn His Thr Asn Leu Gly Arg Lys Asp Asp Glu Lys Phe Tyr Ser
 210 215 220 225

tac cat aaa ctt agc aat aaa ttt aag tgc tat agg tgt cca aca att 956
 Tyr His Lys Leu Ser Asn Lys Phe Lys Ser Tyr Arg Cys Pro Thr Ile
 230 235 240

cga aga ata aga aag tcc atg tgc tcc aaa tac tgg aaa caa gtt cca 1004
 Arg Arg Ile Arg Lys Ser Met Ser Ser Lys Tyr Trp Lys Gln Val Pro
 245 250 255

aaa gat ttt gga tac agt aga gct gat gtg ggt gtg aag act ctt tat 1052
 Lys Asp Phe Gly Tyr Ser Arg Ala Asp Val Gly Val Lys Thr Leu Tyr
 260 265 270

cgc aaa aga aaa tca tgt tat ggt tac aac gca tgg cag cgt gag atc 1100
 Arg Lys Arg Lys Ser Cys Tyr Gly Tyr Asn Ala Trp Gln Arg Glu Ile
 275 280 285

att tat aag aga aga tca cct gac aga agc tgc gtc gta act tct 1148
 Ile Tyr Lys Arg Arg Arg Ser Pro Asp Arg Ser Ser Val Val Thr Ser
 290 295 300 305

gat gga gga ctc agt agt gga agt gtt tcc aag tta ccc aag aag gga	1196
Asp Gly Gly Leu Ser Ser Gly Ser Val Ser Lys Leu Pro Lys Lys Gly	
310 315 320	
gat aca gta aag cta agc att aag tcc ttt agg att cca gag ctt ttt	1244
Asp Thr Val Lys Leu Ser Ile Lys Ser Phe Arg Ile Pro Glu Leu Phe	
325 330 335	
att gaa gtt cca gaa act gca aca gta gga tca cta aag agg act gtg	1292
Ile Glu Val Pro Glu Thr Ala Thr Val Gly Ser Leu Lys Arg Thr Val	
340 345 350	
atg gag gct gtc agt gtt tta ctc agc gga gga ata cgt gtt ggg gtg	1340
Met Glu Ala Val Ser Val Leu Leu Ser Gly Gly Ile Arg Val Gly Val	
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tta atg cat ggg aag aag gtt aga gat gaa agg aaa act ctg tcc cag	1388
Leu Met His Gly Lys Lys Val Arg Asp Glu Arg Lys Thr Leu Ser Gln	
370 375 380 385	
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Thr Gly Ile Ser Cys Asp Glu Asn Leu Asp Asn Leu Gly Phe Thr Leu	
390 395 400	
gag cct agt ccc agc aaa gtt ccc cta cct ttg tgt tct gaa gat cct	1484
Glu Pro Ser Pro Ser Lys Val Pro Leu Pro Leu Cys Ser Glu Asp Pro	
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gct gtg cca acc gac cct aca agt ttg tct gaa cgg tct gcg gcg tct	1532
Ala Val Pro Thr Asp Pro Thr Ser Leu Ser Glu Arg Ser Ala Ala Ser	
420 425 430	
cct atg cta gat tct gga att cca cat gca gat gac gtg att gat tca	1580
Pro Met Leu Asp Ser Gly Ile Pro His Ala Asp Asp Val Ile Asp Ser	
435 440 445	
aga aat att gtg gac agt aac ctc gaa tta gtt cca tat cag ggt gac	1628
Arg Asn Ile Val Asp Ser Asn Leu Glu Leu Val Pro Tyr Gln Gly Asp	
450 455 460 465	
ata tct gtt gat gaa cct tca tca gat tca aaa gag ctt gtc cca ctt	1676
Ile Ser Val Asp Glu Pro Ser Ser Asp Ser Lys Glu Leu Val Pro Leu	
470 475 480	
cca gag ttg gaa gtc aag gcg ctt gcc ata gtt cgg ttg aac cag aaa	1724
Pro Glu Leu Glu Val Lys Ala Leu Ala Ile Val Pro Leu Asn Gln Lys	
485 490 495	
cct aag cgt act gag cta gcc cag agg aga act agg aga ccc ttc tct	1772
Pro Lys Arg Thr Glu Leu Ala Gln Arg Arg Thr Arg Pro Phe Ser	
500 505 510	
gtg aca gag gta gaa gct ctt gta caa gca gtt gag gaa ctc ggg act	1820
Val Thr Glu Val Glu Ala Leu Val Gln Ala Val Glu Glu Leu Gly Thr	
515 520 525	

gga aga tgg cgt gat gta aaa ttg cgt gct ttc gag gat gca gat cat 1868
 Gly Arg Trp Arg Asp Val Lys Leu Arg Ala Phe Glu Asp Ala Asp His
 530 535 540 545

cgg act tac gtg gac ttg aag gac aaa tgg aag acg cta gtt cac aca 1916
 Arg Thr Tyr Val Asp Leu Lys Asp Lys Trp Lys Thr Leu Val His Thr
 550 555 560

gca agt ata tcc cca cag caa cga aga gga gag cgg gtg cca caa gaa 1964
 Ala Ser Ile Ser Pro Gln Gln Arg Arg Gly Glu Pro Val Pro Gln Glu
 565 570 575

ctg cta gac aga gtc ttg agg gca tac ggg tat tgg tcg cag cac caa 2012
 Leu Leu Asp Arg Val Leu Arg Ala Tyr Gly Tyr Trp Ser Gln His Gln
 580 585 590

gga aaa cat cag gcg aga gga gcg tcc aaa gat cca gac atg aac aga 2060
 Gly Lys His Gln Ala Arg Gly Ala Ser Lys Asp Pro Asp Met Asn Arg
 595 600 605

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 Gly Gly Ala Phe Glu Ser Gly Val Ser
 610 615

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agtttaattg tctttatttc tcgttttttt ttttttttct cctacataca cttttttttt 2227

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 35 40 45

Leu Leu Ala Leu Ala Gly Lys Ile Leu Gln Glu Ser Glu Ser Ser Ser
 50 55 60

Ala Ser Ser Asn Ala Phe Glu Glu Ile Lys Gln Glu Lys Val Glu Asn
 65 70 75 80

00110-015000

Cys Lys Thr Ile Lys Ser Glu Ser Ser Asp Gln Gly Asn Ser Val Ser
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 Lys Pro Thr Tyr Asp Ile Ser Thr Glu Lys Cys Val Val Asn Ser Cys
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 Phe Ser Phe Pro Asp Ser Asp Gly Val Leu Glu Arg Thr Pro Met Ser
 115 120 125
 Asp Tyr Lys Lys Ile His Gly Leu Met Asp Val Gly Cys Glu Asn Lys
 130 135 140
 Asn Val Asn Asn Gly Phe Glu Gln Gly Glu Ala Thr Asp Arg Val Gly
 145 150 155 160
 Asp Gly Gly Leu Val Thr Asp Thr Cys Asn Leu Glu Asp Ala Thr Ala
 165 170 175
 Leu Gly Leu Gln Phe Pro Lys Ser Val Cys Val Gly Gly Asp Leu Lys
 180 185 190
 Ser Pro Ser Thr Leu Asp Met Thr Pro Asn Gly Ser Tyr Ala Arg His
 195 200 205
 Gly Asn His Thr Asn Leu Gly Arg Lys Asp Asp Asp Glu Lys Phe Tyr
 210 215 220
 Ser Tyr His Lys Leu Ser Asn Lys Phe Lys Ser Tyr Arg Cys Pro Thr
 225 230 235 240
 Ile Arg Arg Ile Arg Lys Ser Met Ser Ser Lys Tyr Trp Lys Gln Val
 245 250 255
 Pro Lys Asp Phe Gly Tyr Ser Arg Ala Asp Val Gly Val Lys Thr Leu
 260 265 270
 Tyr Arg Lys Arg Lys Ser Cys Tyr Gly Tyr Asn Ala Trp Gln Arg Glu
 275 280 285
 Ile Ile Tyr Lys Arg Arg Arg Ser Pro Asp Arg Ser Ser Val Val Thr
 290 295 300
 Ser Asp Gly Gly Leu Ser Ser Gly Ser Val Ser Lys Leu Pro Lys Lys
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 Gly Asp Thr Val Lys Leu Ser Ile Lys Ser Phe Arg Ile Pro Glu Leu
 325 330 335
 Phe Ile Glu Val Pro Glu Thr Ala Thr Val Gly Ser Leu Lys Arg Thr
 340 345 350
 Val Met Glu Ala Val Ser Val Leu Ser Gly Gly Ile Arg Val Gly
 355 360 365
 Val Leu Met His Gly Lys Lys Val Arg Asp Glu Arg Lys Thr Leu Ser
 370 375 380

Gln Thr Gly Ile Ser Cys Asp Glu Asn Leu Asp Asn Leu Gly Phe Thr
385 390 395 400

Leu Glu Pro Ser Pro Ser Lys Val Pro Leu Pro Leu Cys Ser Glu Asp
405 410 415

Pro Ala Val Pro Thr Asp Pro Thr Ser Leu Ser Glu Arg Ser Ala Ala
420 425 430

Ser Pro Met Leu Asp Ser Gly Ile Pro His Ala Asp Asp Val Ile Asp
435 440 445

Ser Arg Asn Ile Val Asp Ser Asn Leu Glu Leu Val Pro Tyr Gln Gly
450 455 460

Asp Ile Ser Val Asp Glu Pro Ser Ser Asp Ser Lys Glu Leu Val Pro
465 470 475 480

Leu Pro Glu Leu Glu Val Lys Ala Leu Ala Ile Val Pro Leu Asn Gln
485 490 495

Lys Pro Lys Arg Thr Glu Leu Ala Gln Arg Arg Thr Arg Arg Pro Phe
500 505 510

Ser Val Thr Glu Val Glu Ala Leu Val Gln Ala Val Glu Glu Leu Gly
515 520 525

Thr Gly Arg Trp Arg Asp Val Lys Leu Arg Ala Phe Glu Asp Ala Asp
530 535 540

His Arg Thr Tyr Val Asp Leu Lys Asp Lys Trp Lys Thr Leu Val His
545 550 555 560

Thr Ala Ser Ile Ser Pro Gln Gln Arg Arg Gly Glu Pro Val Pro Gln
565 570 575

Glu Leu Leu Asp Arg Val Leu Arg Ala Tyr Gly Tyr Trp Ser Gln His
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 gaagagcaag ttccgaaaaat ggagggcggt cgtgtataga tccaccaccc acagccctg 179
 atg gaa gca gac aac gga ggc ccc aat tct agt cat gca tcc aaa caa 227
 Met Glu Ala Asp Asn Gly Gly Pro Asn Ser Ser His Ala Ser Lys Gln
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 Arg Leu Arg Trp Thr His Glu Leu His Glu Arg Phe Val Asp Ala Val
 20 25 30
 gct caa ctt ggt ggc cct gat aga gct aca ccc aaa ggc gtt ctt aga 323
 Ala Gln Leu Gly Gly Pro Asp Arg Ala Thr Pro Lys Gly Val Leu Arg
 35 40 45
 gtg atg ggt gta caa ggc tta act ata tat cat gtc aag agt cac tta 371
 Val Met Gly Val Gln Gly Leu Thr Ile Tyr His Val Lys Ser His Leu
 50 55 60
 cag aaa tat cga ctt gca aag tat ctt cca gat tcg tct tct gaa ggg 419
 Gln Lys Tyr Arg Leu Ala Lys Tyr Leu Pro Asp Ser Ser Ser Glu Gly
 65 70 75 80
 aaa aaa act gat aag aaa gaa tct gga gat atg ctc tct ggg ttg gac 467
 Lys Lys Thr Asp Lys Lys Glu Ser Gly Asp Met Leu Ser Gly Leu Asp
 85 90 95
 ggc tcg tcg gga atg cag ata act gaa gcc ctc aag ttg cag atg gaa 515
 Gly Ser Ser Gly Met Gln Ile Thr Glu Ala Leu Lys Leu Gln Met Glu
 100 105 110
 gtt cag aaa cga ttg cac gag caa cta gaa gtg caa aga cag ctg caa 563
 Val Gln Lys Arg Leu His Glu Gln Leu Glu Val Gln Arg Gln Leu Gln
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 130 135 140
 caa caa cga ctc agt gga gta ctc ggc gaa ccc tca gcc cca gta acg 659
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 Gly Asp Ser Asp Pro Ala Thr Pro Ala Pro Thr Ser Glu Ser Pro Leu
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 caa gac aag tct ggc aag gac tgt gga cca gac aaa agt ctc tca gtt 755
 Gln Asp Lys Ser Gly Lys Asp Cys Gly Pro Asp Lys Ser Leu Ser Val
 180 185 190
 gac gag tct ctc tca tct tac cgg gag cct tta aca cca gac tca ggg 803
 Asp Glu Ser Leu Ser Ser Tyr Arg Glu Pro Leu Thr Pro Asp Ser Gly
 195 200 205

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Cys Asn Ile Gly Ser Pro Asp Glu Ser Thr Gly Glu Glu Arg Leu Ser	
210 215 220	
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Lys Lys Pro Arg Leu Val Arg Gly Ala Ala Gly Tyr Thr Pro Asp Ile	
225 230 235 240	
gta gtg ggt cac cca ata cta gaa tca ggc ttg aac act tct tac cat	947
Val Val Gly His Pro Ile Leu Glu Ser Gly Leu Asn Thr Ser Tyr His	
245 250 255	
cag tca gac cat gtc ctc gcc ttt gac cag cca tct aca tca ctg ctt	995
Gln Ser Asp His Val Leu Ala Phe Asp Gln Pro Ser Thr Ser Leu Leu	
260 265 270	
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Gly Ala Glu Glu Gln Leu Asp Lys Val Ser Gly Asp Asn Leu	
275 280 285	
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Val Met Gly Val Gln Gly Leu Thr Ile Tyr His Val Lys Ser His Leu	
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Gln Lys Tyr Arg Leu Ala Lys Tyr Leu Pro Asp Ser Ser Ser Glu Gly	
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Lys Lys Thr Asp Lys Lys Glu Ser Gly Asp Met Leu Ser Gly Leu Asp	
85 90 95	
Gly Ser Ser Gly Met Gln Ile Thr Glu Ala Leu Lys Leu Gln Met Glu	
100 105 110	

Val Gln Lys Arg Leu His Glu Gln Leu Glu Val Gln Arg Gln Leu Gln
115 120 125

Leu Arg Ile Glu Ala Gln Gly Lys Tyr Leu Lys Lys Ile Ile Glu Glu
130 135 140

Gln Gln Arg Leu Ser Gly Val Leu Gly Glu Pro Ser Ala Pro Val Thr
145 150 155 160

Gly Asp Ser Asp Pro Ala Thr Pro Ala Pro Thr Ser Glu Ser Pro Leu
165 170 175

Gln Asp Lys Ser Gly Lys Asp Cys Gly Pro Asp Lys Ser Leu Ser Val
180 185 190

Asp Glu Ser Leu Ser Ser Tyr Arg Glu Pro Leu Thr Pro Asp Ser Gly
195 200 205

Cys Asn Ile Gly Ser Pro Asp Glu Ser Thr Gly Glu Glu Arg Leu Ser
210 215 220

Lys Lys Pro Arg Leu Val Arg Gly Ala Ala Gly Tyr Thr Pro Asp Ile
225 230 235 240

Val Val Gly His Pro Ile Leu Glu Ser Gly Leu Asn Thr Ser Tyr His
245 250 255

Gln Ser Asp His Val Leu Ala Phe Asp Gln Pro Ser Thr Ser Leu Leu
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275 280 285

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<222> (112)..(987)

<223> G1197

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<223> "n" at various positions throughout the sequence
may be A, T, C, G, other or unknown

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Met Tyr

1

tcg gcg att cgg tct tcg ctt cct cta gat ggc agc ttg gga gac tac	165
Ser Ala Ile Arg Ser Ser Leu Pro Leu Asp Gly Ser Leu Gly Asp Tyr	
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tct gac gga acc aat ctt ccc atc gac gct tgt ctg gtc cta acc act	213
Ser Asp Gly Thr Asn Leu Pro Ile Asp Ala Cys Leu Val Leu Thr Thr	
20 25 30	
gac ccc aag cct cgc ctt cgt tgg acc tct gag ctc cat gaa aga ttc	261
Asp Pro Lys Pro Arg Leu Arg Trp Thr Ser Glu Leu His Glu Arg Phe	
35 40 45 50	
gtt gac gcc gtc act cag ctc ggc gga ccc gac aaa gca acg cct aaa	309
Val Asp Ala Val Thr Gln Leu Gly Gly Pro Asp Lys Ala Thr Pro Lys	
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Ser Ile Asp Asn Ser Thr Ser Cys Val Ala Glu Ser Gln Asp	
100 105 110	
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Thr Gly Ser Ser Ser Thr Ser Ser Leu Arg Leu Ala Ala Gln Glu Gln	
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Gln Arg Arg Leu His Glu Gln Leu Glu Val Gln Arg Arg Leu Gln Leu	
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Arg Ile Glu Ala Gln Gly Lys Tyr Leu Gln Ser Ile Leu Glu Lys Ala	
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Cys Lys Ala Ile Glu Glu Gln Ala Val Ala Phe Ala Gly Leu Glu Ala	
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Ala Arg Glu Glu Leu Ser Glu Leu Ala Ile Lys Ala Ser Ile Thr Asn	
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Gly Cys Gln Gly Thr Thr Ser Thr Phe Asp Thr Thr Lys Met Met Ile	
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Pro Ser Leu Ser Glu Leu Ala Val Ala Ile Glu His Lys Asn Asn Cys	
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Ser Ala Glu Ser Ser Leu Thr Ser Ser Thr Val Gly Ser Pro Val Ser	
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Ala Ala Leu Met Lys Lys Arg Gln Arg Gly Val Phe Gly Asn Gly Asp	
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Arg Phe Val Asp Ala Val Thr Gln Leu Gly Gly Pro Asp Lys Ala Thr	
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Pro Lys Thr Ile Met Arg Thr Met Gly Val Lys Gly Leu Thr Leu Tyr	
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His Leu Lys Ser His Leu Gln Lys Phe Arg Leu Gly Arg Gln Ser Cys	
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Lys Glu Ser Ile Asp Asn Ser Lys Asp Val Ser Cys Val Ala Glu Ser	
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 Glu Val Gln Arg Arg Leu His Glu Gln Leu Glu Val Gln Arg Arg Leu
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